

La bioinformatica come disciplina trasversale a sostegno delle scienze agrarie

Nunzio D'Agostino

nunzio.dagostino@unina.it





OUTLINE

- LA MIA STORIA
- BIG DATA E SCIENZE OMICHE
- BIOINFORMATICA: DEFINIZIONE E SCOPI
- ALCUNE MIE ESPERIENZE DI RICERCA



LA MIA STORIA FORMATIVA E PROFESSIONALE



1997-2002 SIENA
UNIVERSITÀ DEGLI STUDI DI SIENA
LAUREA IN SCIENZE BIOLOGICHE
INDIRIZZO BIOMOLECOLARE



Streptococcus agalactiae



Identification of a Universal Group B *Streptococcus* Vaccine by Multiple Genome Screen

Domenico Maione,^{1*} Immaculada Margarit,^{1*}
Cira D. Rinaudo,¹ Vega Massignani,¹ Marirosa Mora,¹
Maria Scarselli,¹ Hervé Tettelin,² Cecilia Brettoni,¹
Emilia T. Iacobini,¹ Roberto Rosini,¹ Nunzio D'Agostino,¹
Lisa Miorin,¹ Scilla Buccato,¹ Massimo Mariani,¹ Giuliano Galli,¹
Renzo Nogarotto,¹ Vincenzo Nardi Dei,¹ Filippo Vegni,¹
Claire Fraser,² Giuseppe Mancuso,³ Giuseppe Teti,³
Lawrence C. Madoff,⁴ Lawrence C. Paoletti,⁴ Rino Rappuoli,¹
Dennis L. Kasper,⁴ John L. Telford,¹ Guido Grandi^{1†}

Science. 2005;309(5731):148-150



LA MIA STORIA FORMATIVA E PROFESSIONALE



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INDIRIZZO BIOMOLECOLARE

2002-2003 ARIANO IRPINO (AV)
UNIVERSITÀ DEGLI STUDI DEL SANNIO
MASTER DI II LIVELLO IN BIOINFORMATICA





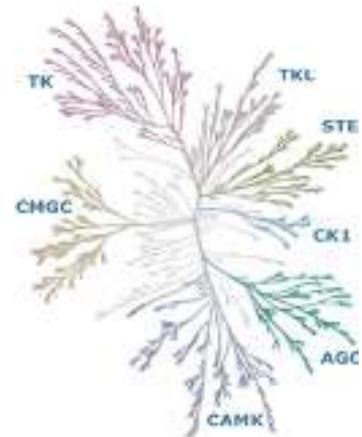
LA MIA STORIA FORMATIVA E PROFESSIONALE



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INDIRIZZO BIOMOLECOLARE

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MASTER DI II LIVELLO IN BIOINFORMATICA

2003-2004 MILANO
CNR-ITB
ASSEGNO DI RICERCA



BMC Bioinformatics



Research article

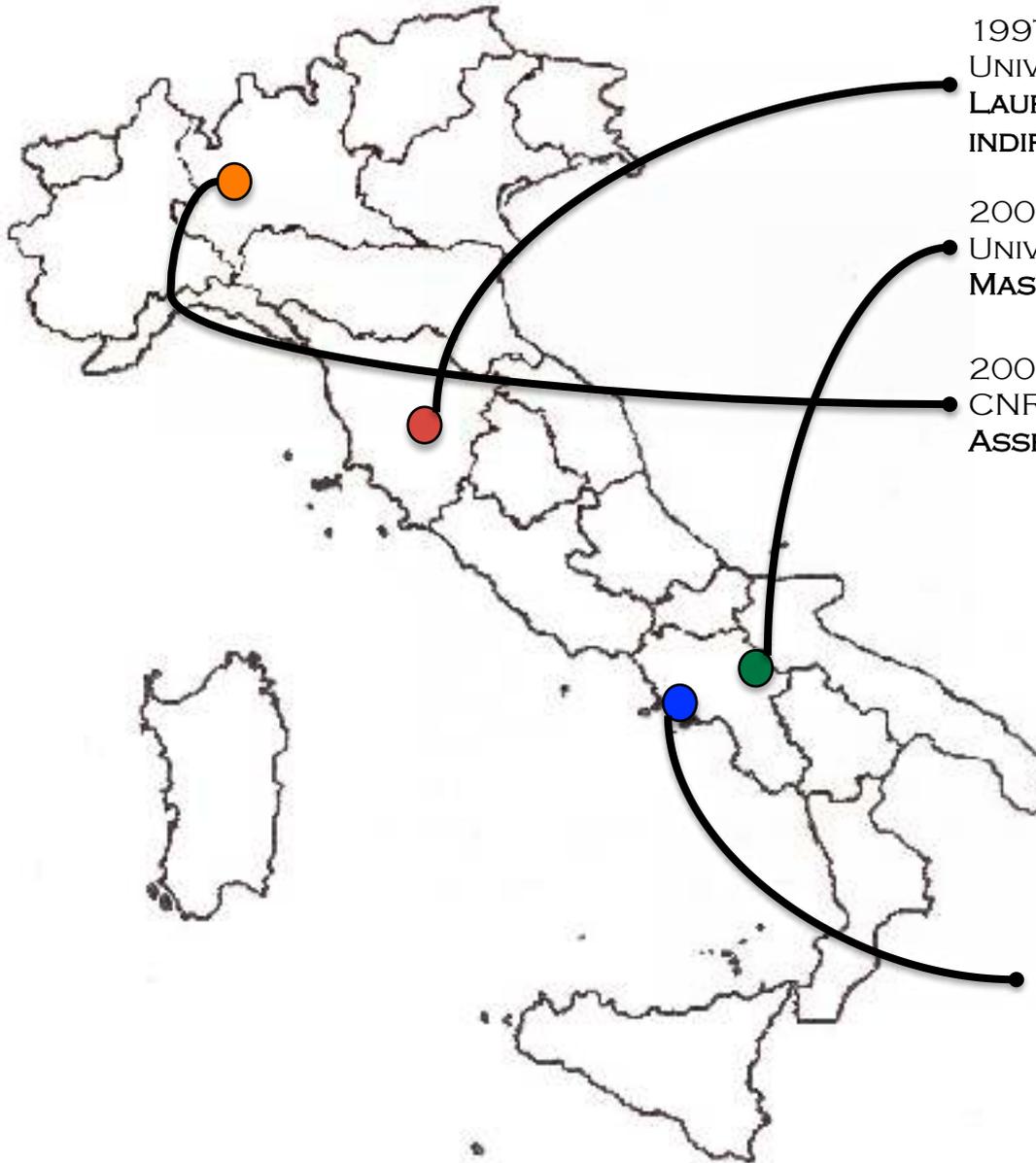
Open Access

Systematic analysis of human kinase genes: a large number of genes and alternative splicing events result in functional and structural diversity

Luciano Milanesi^{1,2}, Mauro Petrillo³, Leandra Sepe^{4,1}, Angelo Bocchia⁵,
Nunzio D'Agostino¹, Vyriam Passamano¹, Salvatore Di Nardo¹,
Gianluca Tasco^{1,3}, Rita Casadio² and Giovanni Paoletta^{3,4,6}



LA MIA STORIA FORMATIVA E PROFESSIONALE



1997-2002 SIENA
UNIVERSITÀ DEGLI STUDI DI SIENA
LAUREA IN SCIENZE BIOLOGICHE
INDIRIZZO BIOMOLECOLARE

2002-2003 ARIANO IRPINO (AV)
UNIVERSITÀ DEGLI STUDI DEL SANNIO
MASTER DI II LIVELLO IN BIOINFORMATICA

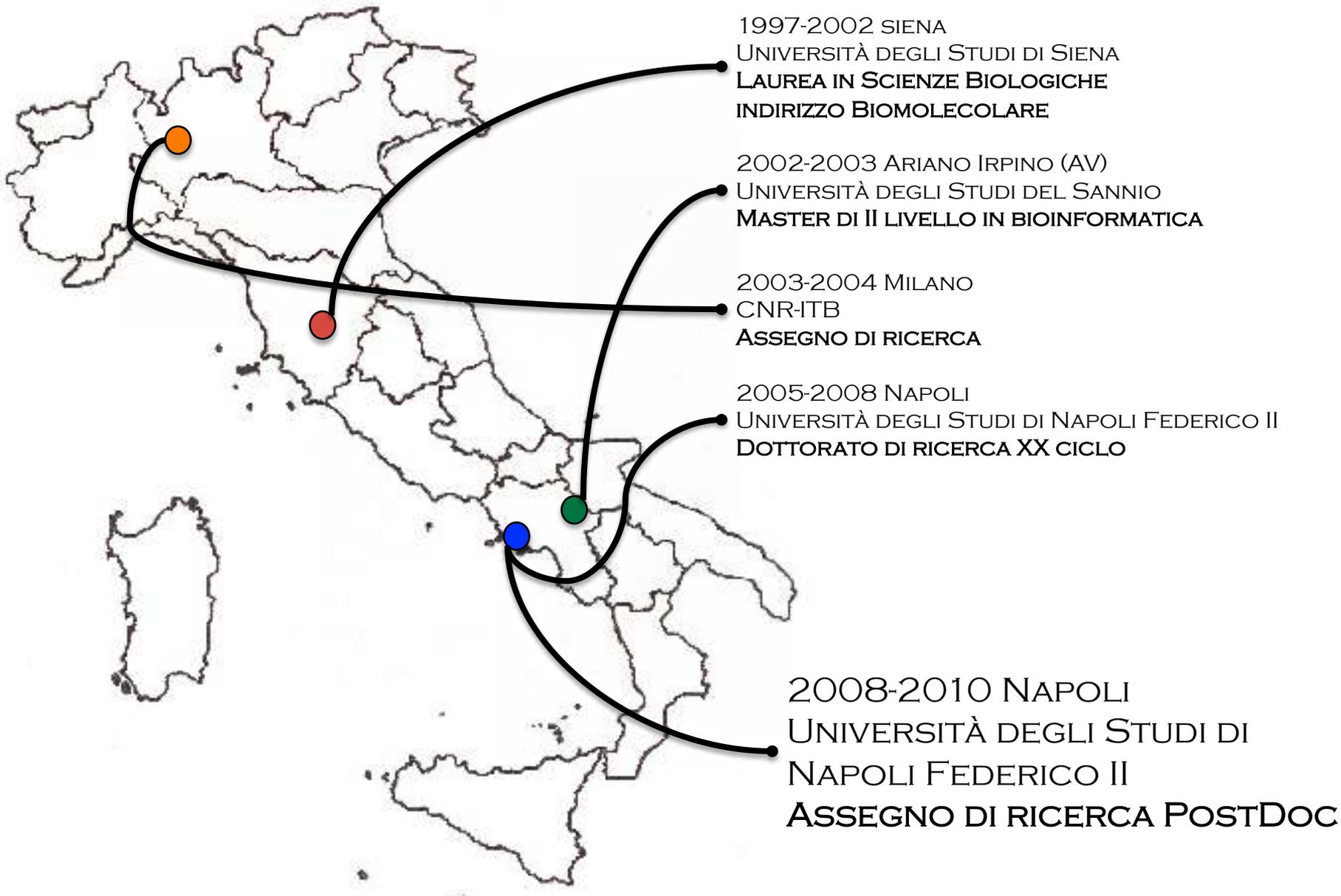
2003-2004 MILANO
CNR-ITB
ASSEGNO DI RICERCA

2005-2008 NAPOLI
UNIVERSITÀ DEGLI STUDI DI
NAPOLI FEDERICO II
DOTTORATO DI RICERCA XX CICLO



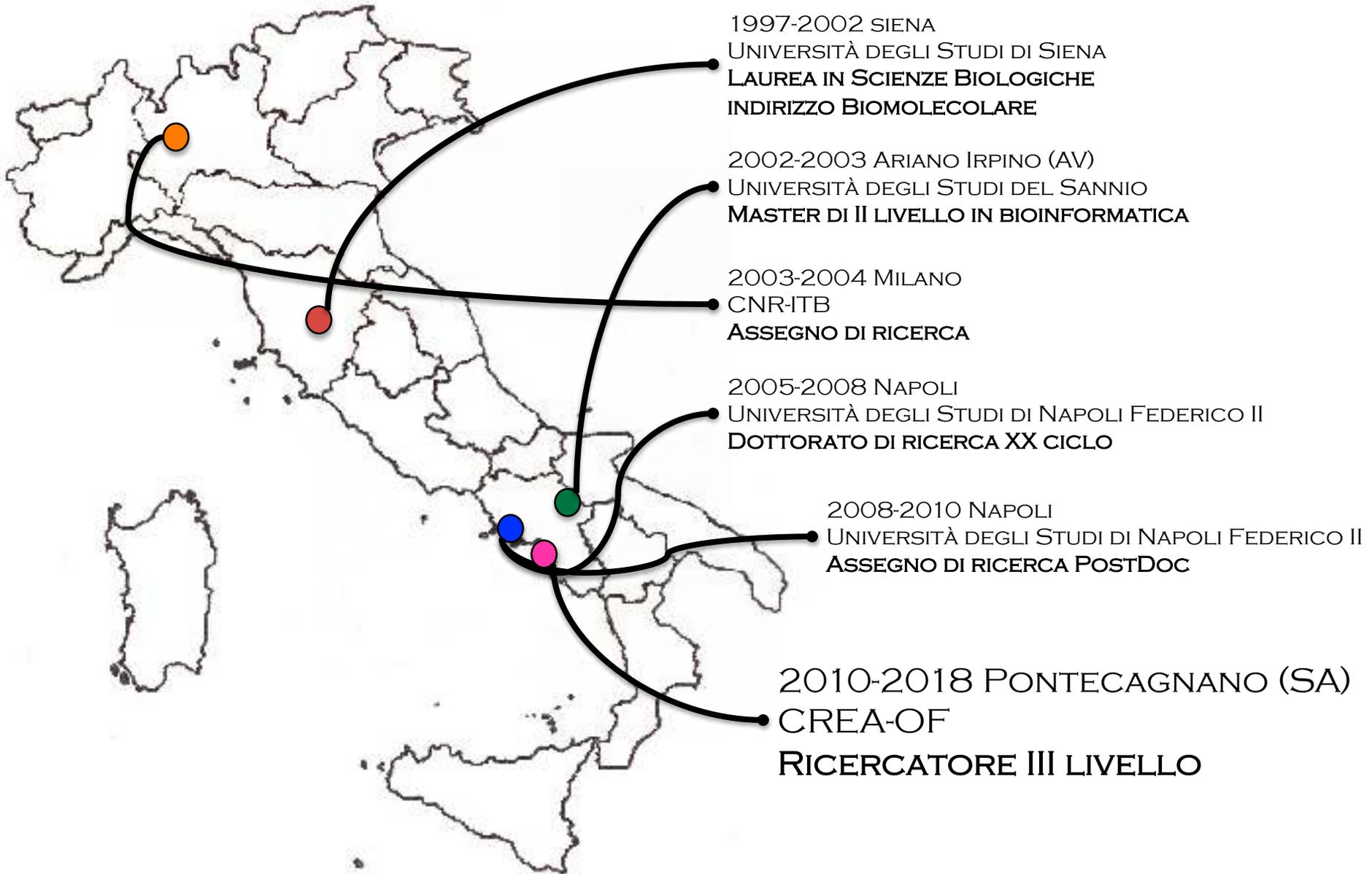


LA MIA STORIA FORMATIVA E PROFESSIONALE





LA MIA STORIA FORMATIVA E PROFESSIONALE



LA MIA STORIA FORMATIVA E PROFESSIONALE

Plant Appl Genet
DOI 10.1007/s00343-011-0199-7

ORIGINAL PAPER

Comparative next-generation mapping of the *Phytophthora infestans* resistance gene *Rpi-dlc2* in a European accession of *Solanum dulcamara*

T. M. Colas · H. van de Geest · J. Gros ·
A. Silakova · N. D'Agostino · J. P. Nap ·
C. Mariani · J. J. B. M. Allés · I. Rieu

D'Agostino et al. BMC Genomics 2011
<http://www.biomedcentral.com/1471>

Plant, Cell &
Environment

Plant, Cell and Environment (2016)

PC
E

doi:10.1111/pcpe.12070

Original Article

Drought and flooding have distinct effects on herbivore-induced responses and resistance in *Solanum dulcamara*

Duy Nguyen¹, Nunzio D'Agostino², Tom O.G. Tytgat¹, Pulu Sun^{1,2}, Tobias Lortzing¹, Eric J. W. Visser¹, Simona M. Cristescu¹, Anke Steppuhn², Celestina Mariani¹, Nicolai M. van Duin^{1,2} & Ivo Rieu¹

RESEARCH ARTICLE

Open Access

Genomic analysis of the native European *Solanum* species, *S. dulcamara*

Nunzio D'Agostino^{1,2}, Tomek Colas^{1,2*}, Henri van de Geest^{1,2}, Aureliano Bombarely⁴, Thikra Darwood¹, Jan Zethof¹, Nicky Driedonks¹, Erik Wijnker², Joachim Bargsten¹, Jan-Peter Nap^{1,2}, Celestina Mariani^{1,2} and Ivo Rieu¹



FEB - AGO 2012 NIJMEGEN
Radboud University
DEPT. OF MOLECULAR PLANT
PHYSIOLOGY
VISITING SCIENTIST





LA MIA STORIA FORMATIVA E PROFESSIONALE

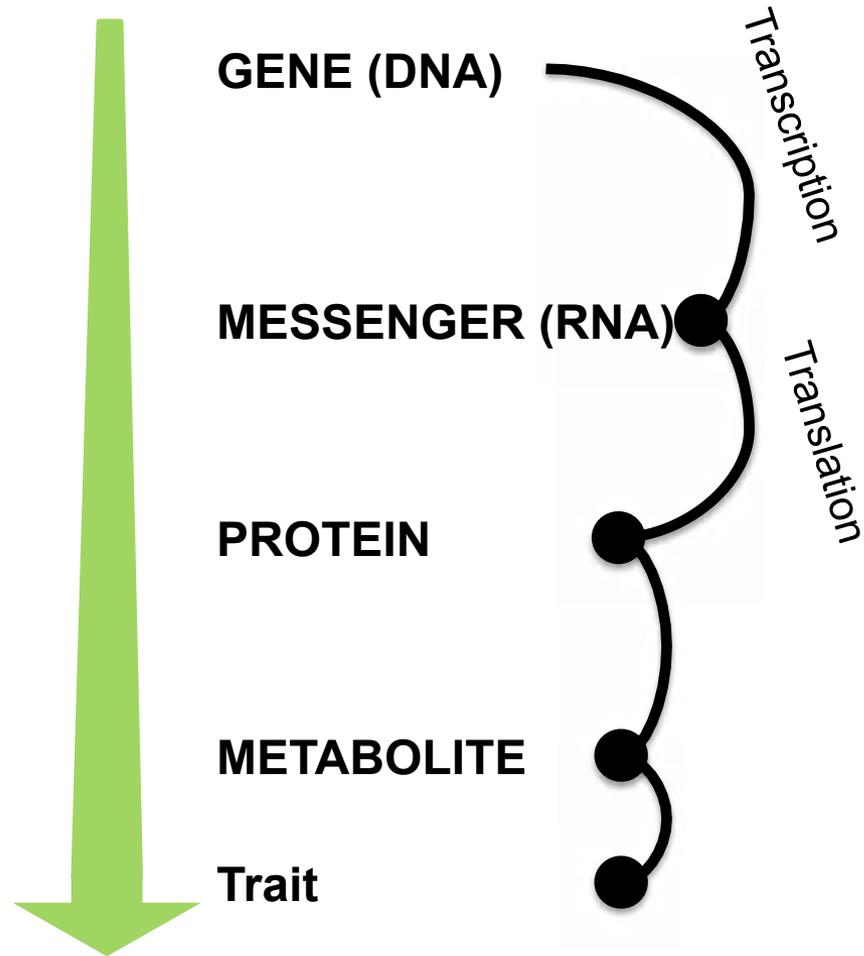


DA DICEMBRE 2018 RTD-B SSD BIO 11 (BIOLOGIA MOLECOLARE)



IL DOGMA CENTRALE DELLA BIOLOGIA MOLECOLARE

*Genotype (i.e. **Aa**)*



Phenotype (red flower)



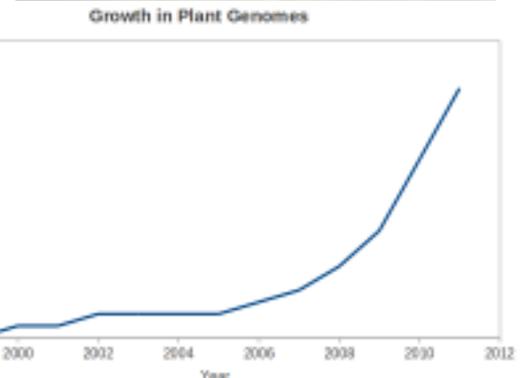
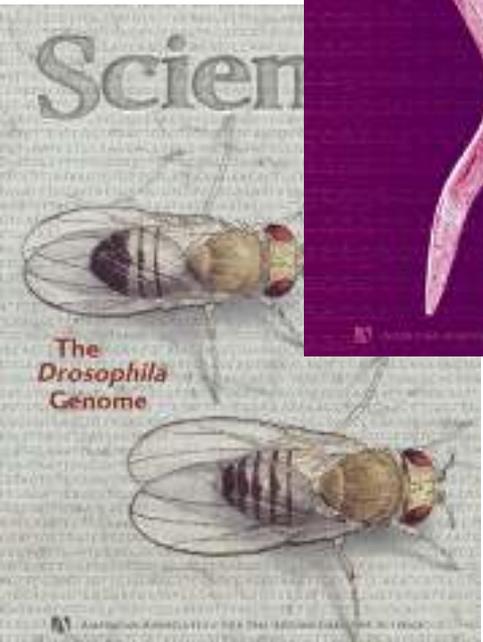
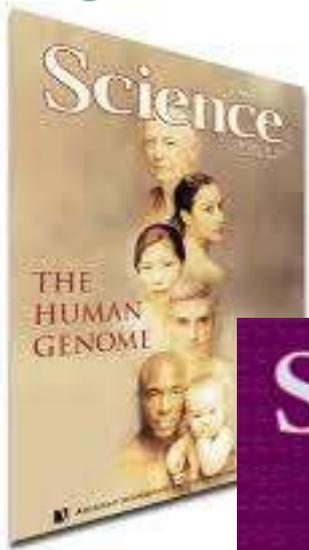
IL SEQUENZIAMENTO DEL DNA

La sequenza del DNA può rivelarci...

- tutto sulla vita di un organismo
- il suo programma di sviluppo
- il suo funzionamento
- resistenza o suscettibilità alle malattie
- quanto sia simili agli altri organismi

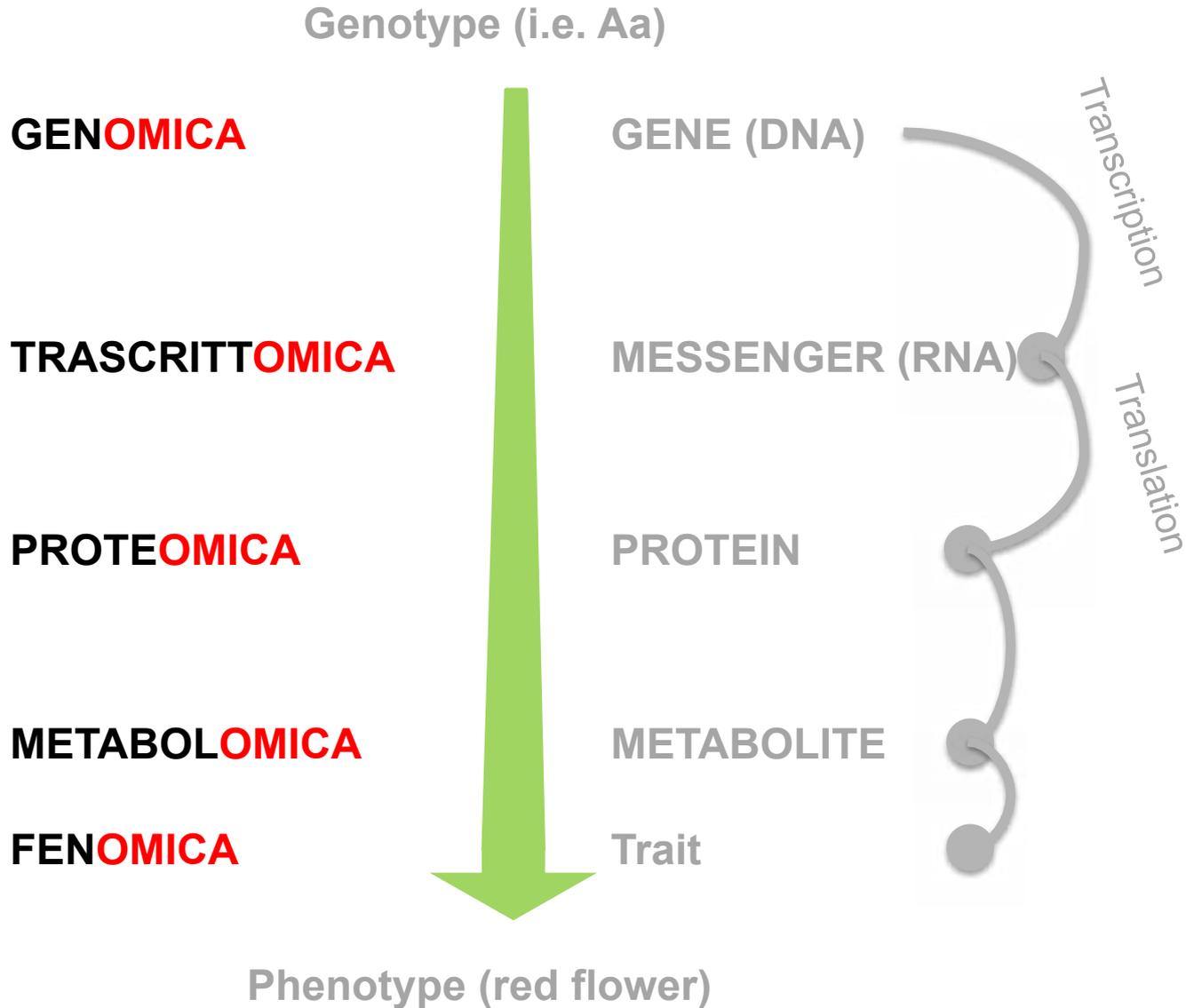


IL SEQUENZIAMENTO DEL DNA





THE OMICS CASCADE





LE SCIENZE OMICHE

The Wholeness in Suffix *-omics*, *-omes*, and the Word *Om*

Satya P. Yadav *Journal of biomolecular techniques : JBT* vol. 18,5 (2007): 277.



*omics

Google Search

I'm Feeling Lucky

829 words





THE OMICS REVOLUTION

Omic methods are not only defined

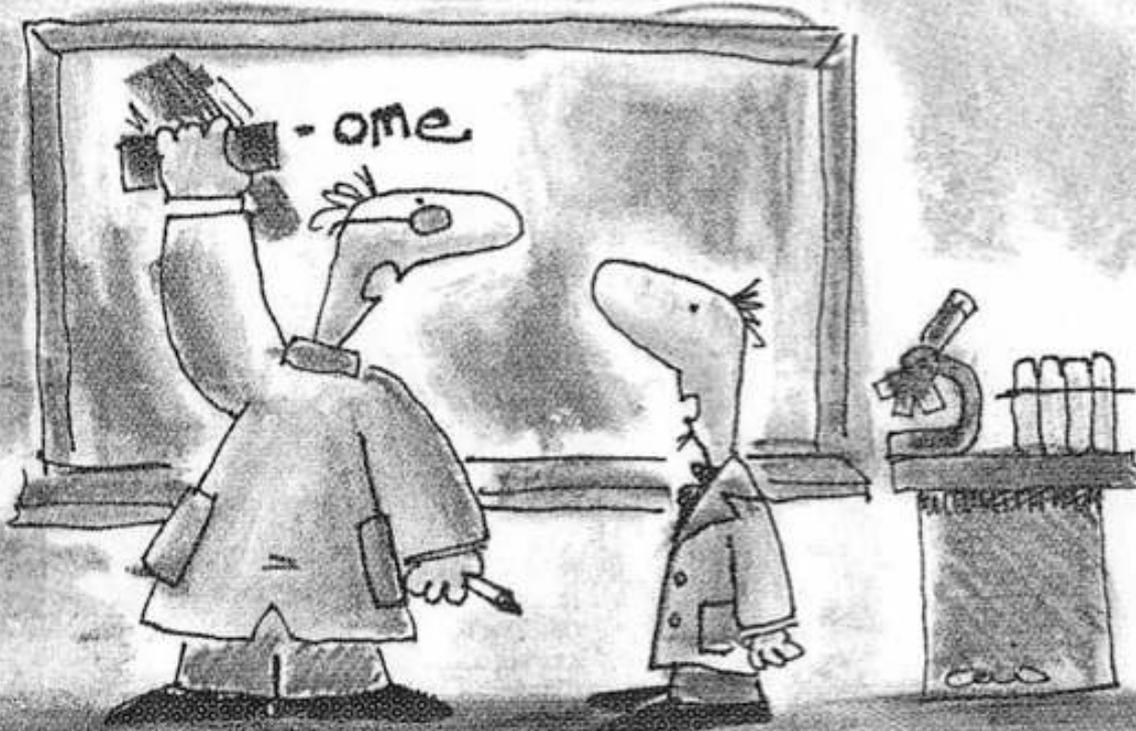
by HIGH THROUGH-PUT...

...but also by **HIGH OUT-PUT!**



LE SCIENZE OMICHE

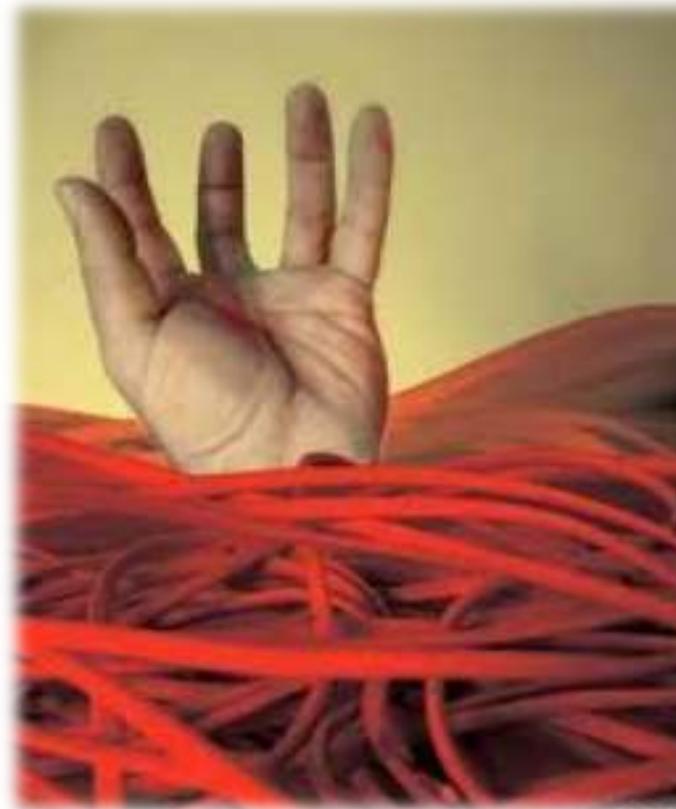
How do you define success in science?



When I coin my own "-ome" word.



SEPOLTI DAI DATI



**Stiamo nuotando in un mare di dati in rapido aumento. . .
come possiamo evitare di affogare?**



La bioinformatica non è separata dalla biologia molecolare:

la conoscenza e la comprensione della biologia molecolare è condizione necessaria per applicare in maniera efficace la bioinformatica



COS'È LA BIOINFORMATICA?

Il termine **bioinformatica** è stato introdotto nel 1970 da Paulien Hogeweg per fare riferimento allo studio dei **processi di informazione nei sistemi biotici**.

Simulating the growth of cellular forms

PAULINE HOGEWEG received her university education at the University of Amsterdam (doctoral degree in 1969, major in biology). In 1978 she received her doctorate degree from the University of Utrecht (thesis: Topics in Biological Pattern Analysis). Since 1970 she has been a staff member at the Subfaculty of Biology of the University of Utrecht, with her main field of research in bioinformatics. Her major interests include pattern generation and pattern recognition.

INTRODUCTION

Organisms grow and develop their characteristic form by repeated cell divisions. It may be assumed that this process is regulated by the state of the individual cells and their interactions with cells adjacent

by
Pauline Hogeweg
Bioinformatica
Subfaculty of Biology
University of Utrecht
Padualaan 8
Utrecht, the Netherlands



to them, that is, in wall-to-wall or wall-fluid contact with them. The myriad patterns of intricate delicacy apparent in the development of plants and animals may seem to us marvelously complex; yet it is conceivable that such growth patterns may be generated by relatively simple rules which in the case of organisms we assume to be encoded in each cell's DNA. Current views attribute a small number of possible states to a cell and specify its transitions to other allowed states as a function of the state of the individual cell and the states of its *informationally adjacent* neighbours (i.e., those that affect it).⁹

The study of cellular growth models is an emerging field called *cellular axology*,⁹ and its principal investigative tool is observing the behaviour of the



SEPTEMBER 1978



COS'È LA BIOINFORMATICA?

Review Paper

N.M. Luscombe,
D. Greenbaum,
M. Gerstein

Department of Molecular Biophysics
and Biochemistry
Yale University
New Haven, USA

Review

What is bioinformatics? An introduction and overview

Abstract A flood of data means that many of the challenges in biology are now challenges in computing. Bioinformatics, the application of computational techniques to analyse the information associated with biomolecules on a large scale, has now firmly established

Bioinformatics - a definition¹

(*Molecular*) **bio** – informatics: bioinformatics is conceptualising biology in terms of molecules (in the sense of physical chemistry) and applying "informatics techniques" (derived from disciplines such as applied maths, computer science and statistics) to understand and organise the information associated with these molecules, on a large scale. In short, bioinformatics is a management information system for molecular biology and has many practical applications.

¹ As submitted to the Oxford English Dictionary



COS'È LA BIOINFORMATICA?

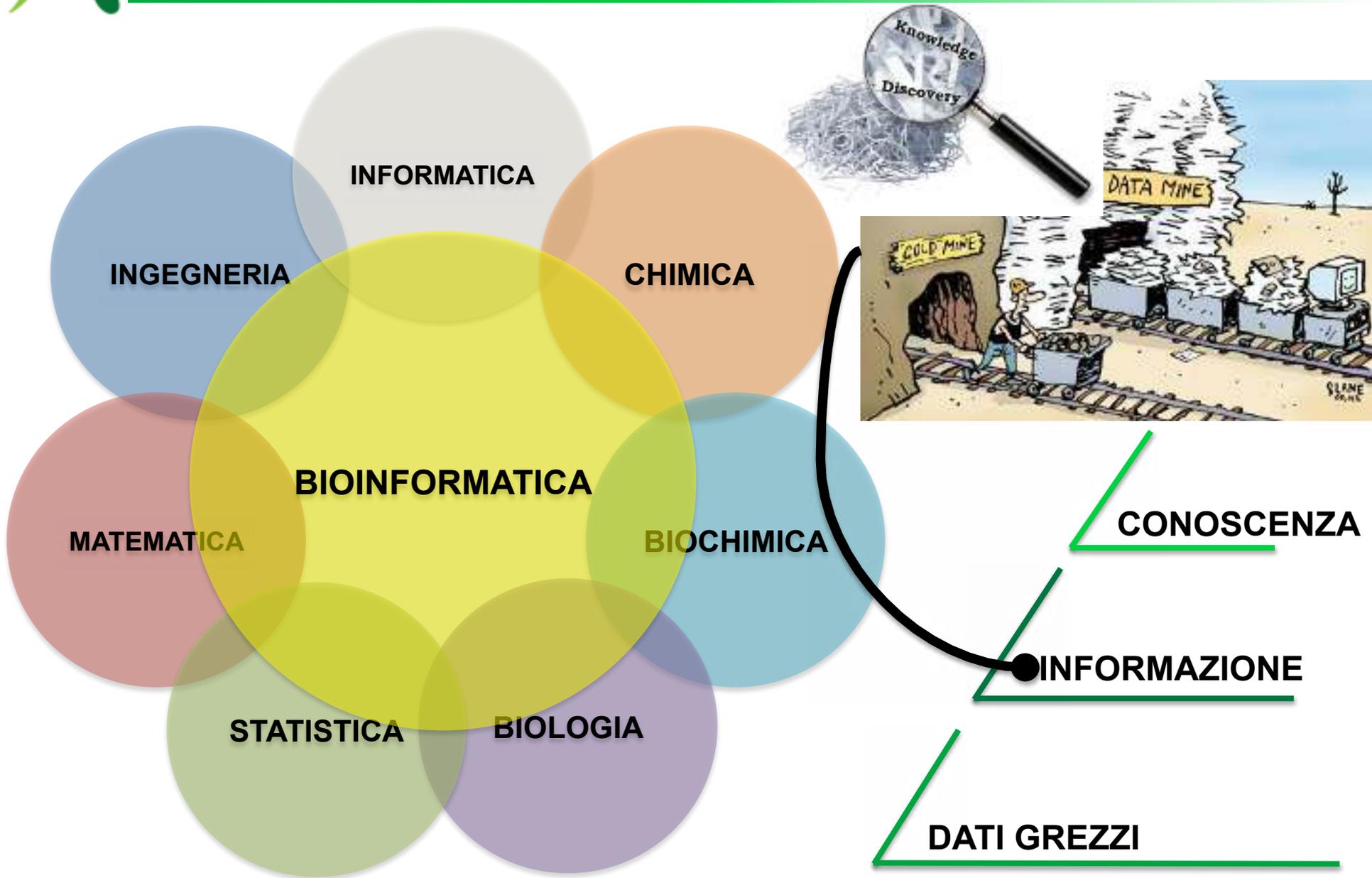


WIKIPEDIA
The Free Encyclopedia

Bioinformatics is an **interdisciplinary** field that develops and improves upon methods for storing, retrieving, organizing and analyzing biological data.

A major activity in bioinformatics is to develop software tools **to generate useful biological knowledge.**

SCIENZA INTERDISCIPLINARE E TRASVERSALE





LA BIOINFORMATICA È

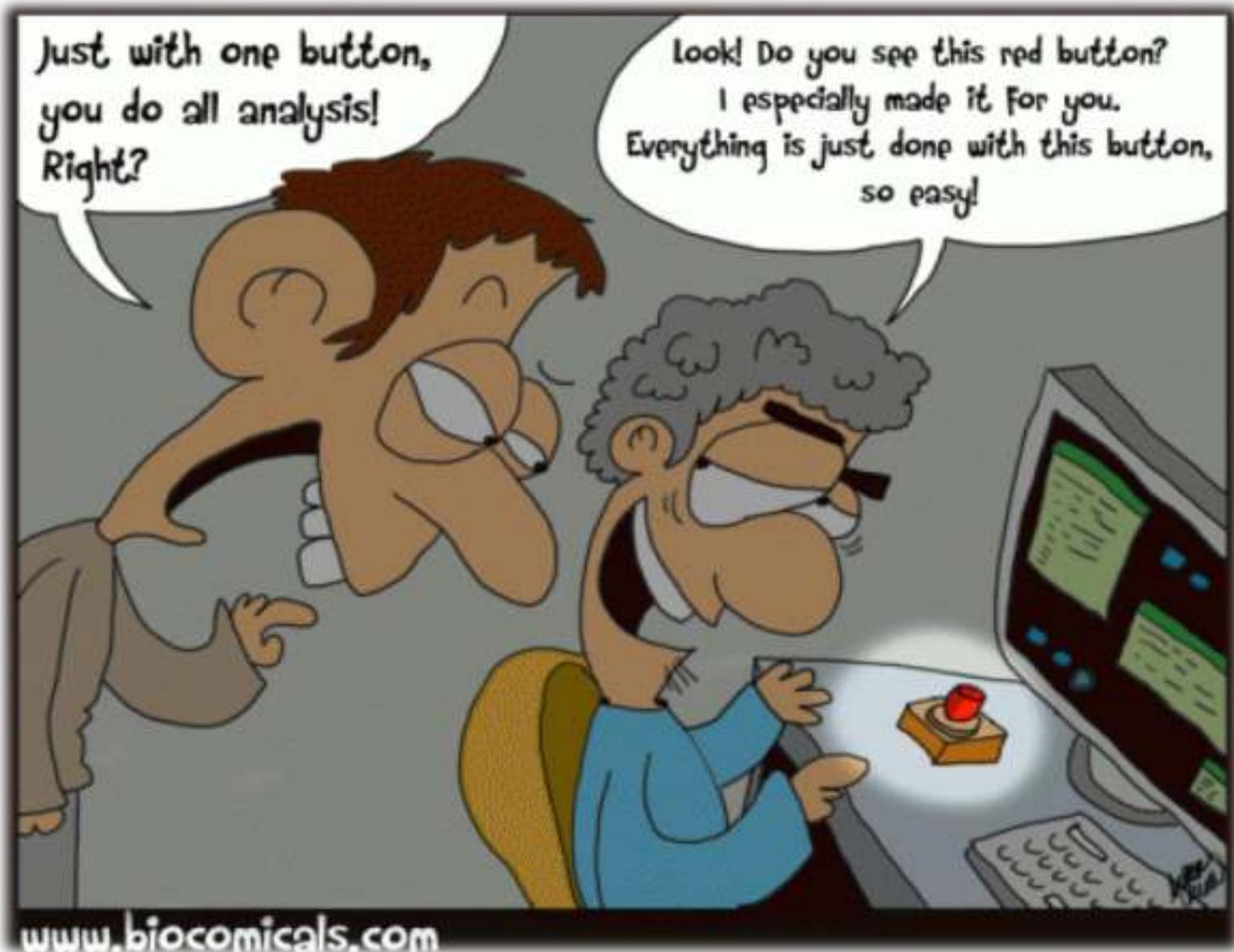
È importante avere un'idea di quali tipi di cose sono possibili o impossibili da ottenere ricorrendo all'utilizzo di approcci bioinformatici.

La bioinformatica è:

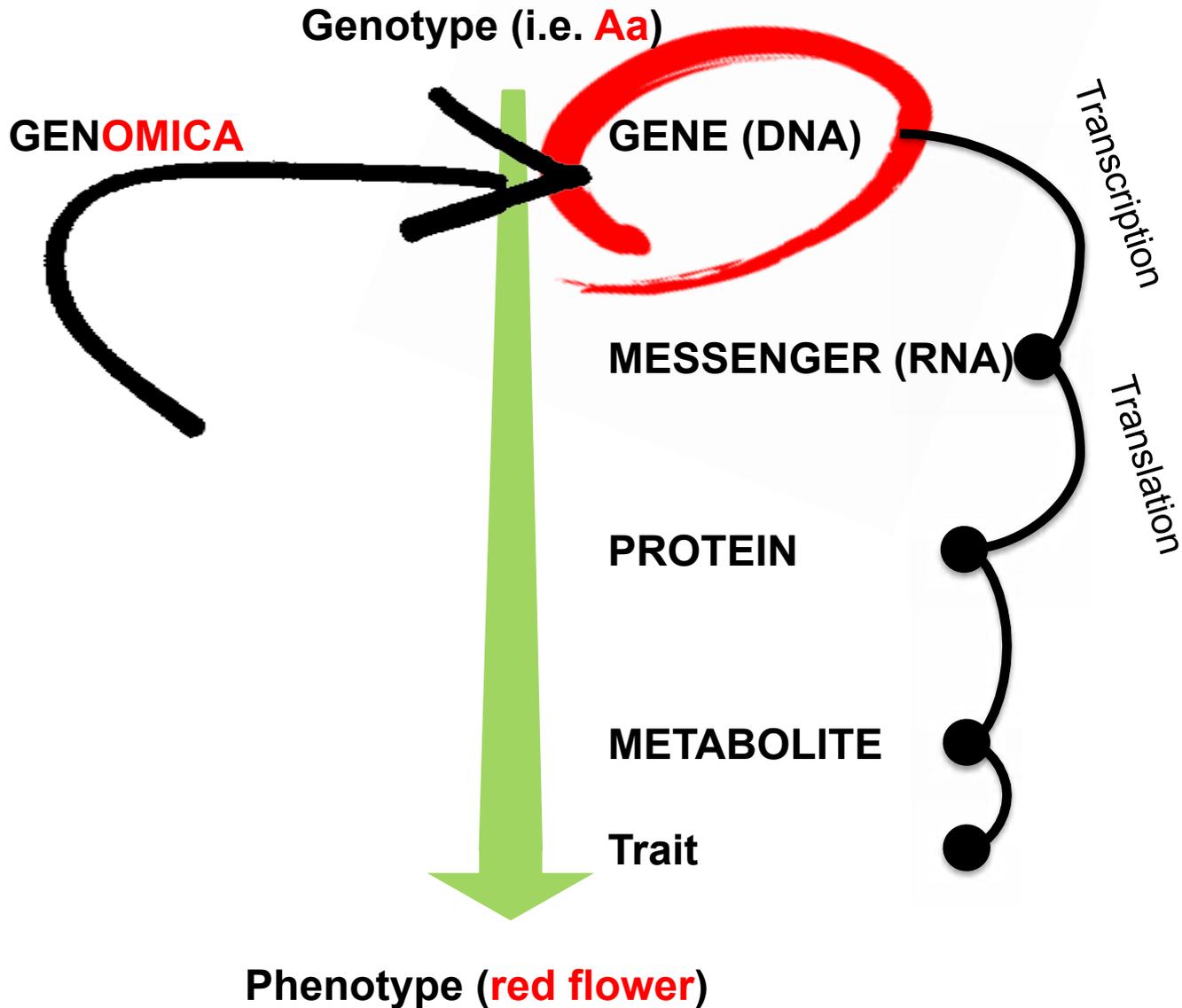
- **a volte un risparmio di tempo**
- **a volte essenziale**
- **a volte non è utile/importante**
- **a volte non applicabile**



LA BIOINFORMATICA E IL PULSANTE ROSSO



IL DOGMA CENTRALE DELLA BIOLOGIA MOLECOLARE





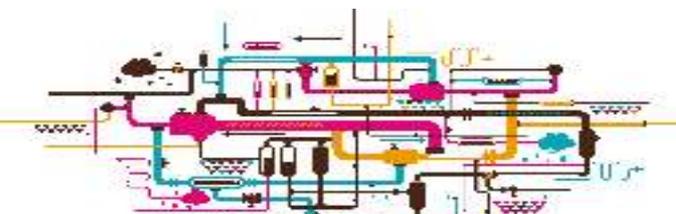
IL GENOMA DEL POMODORO



The tomato genome sequence provides insights into fleshy fruit evolution

The Tomato Genome Consortium*

Il mio compito: membro dell' iTAG (international Tomato Annotation Group)



Published online 16 November 2006

Nucleic Acids Research, 2007, Vol. 35, Database 6



TomatEST database: *in silico* exploitation of EST data to explore expression patterns in tomato species

Nunzio D'Agostino, Mario Aversano, Luigi Frusciantè¹ and Maria Luisa Chiusano*

[Open Access](#)

BMC Bioinformatics

Research article

ParPEST: a pipeline for EST data analysis based on parallel computing

Nunzio D'Agostino, Mario Aversano and Maria Luisa Chiusano*

Research

[Open Access](#)

Gene models from ESTs (GeneModelEST): an application on the *Solanum lycopersicum* genome

Nunzio D'Agostino¹, Alessandra Traini¹, Luigi Frusciantè² and Maria Luisa Chiusano*¹

BMC Plant Biology



Database

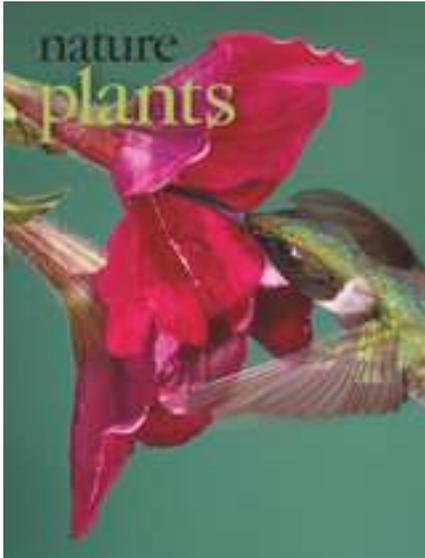
[Open Access](#)

SoIEST database: a "one-stop shop" approach to the study of *Solanaceae* transcriptomes

Nunzio D'Agostino, Alessandra Traini, Luigi Frusciantè and Maria Luisa Chiusano*



IL GENOMA DI PETUNIA



nature
plants

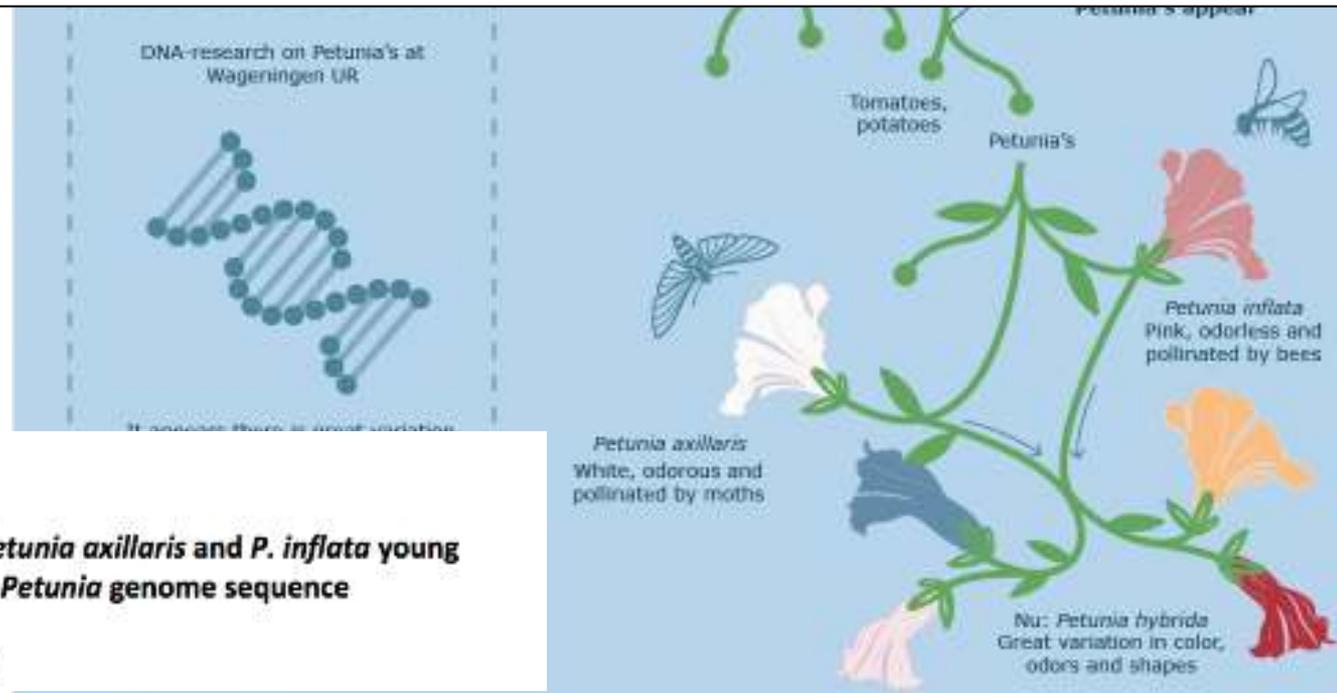
ARTICLES

PUBLISHED: 27 MAY 2016 | ARTICLE NUMBER: 16074 | DOI: 10.1038/NPLANTS.2016.74

OPEN

Insight into the evolution of the Solanaceae from the parental genomes of *Petunia hybrida*

Il mio compito: identificazione ed annotazione dei microRNA



Supplementary Note 9

Identification of conserved miRNAs in *Petunia axillaris* and *P. inflata* young flower buds and their verification in the *Petunia* genome sequence

Kitty Vijverberg^{1,2*}, Nunzio D'Agostino³, Tom Gerats¹



Una strategia alternativa al sequenziamento completo del DNA consiste nel **generare una rappresentazione ridotta del genoma**.

La riduzione del genoma può essere ottenuta usando strategie di arricchimento mirate (***target enrichment***) che consistono nell'isolamento di specifici loci genomici.

Whole genome (100 %)



900 Mb



Exome (2%)



20 Mb



Target (0.55%)



5 Mb





ARRICCHIMENTO E CATTURA DI REGIONI BERSAGLIO (I)

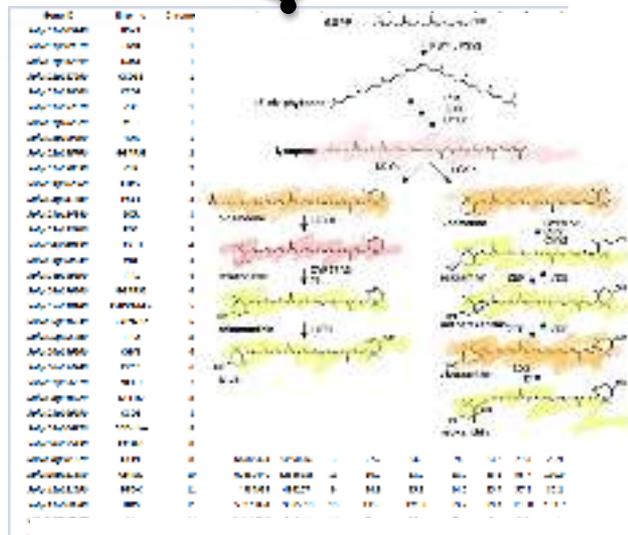
Liquid-phase sequence capture and targeted re-sequencing revealed novel polymorphisms in tomato genes belonging to the MEP carotenoid pathway

Irma Terracciano, Concita Cantarella, Carlo Fasano, Teodoro Cardì, Giuseppe Mennella & Nunzio D'Agostino

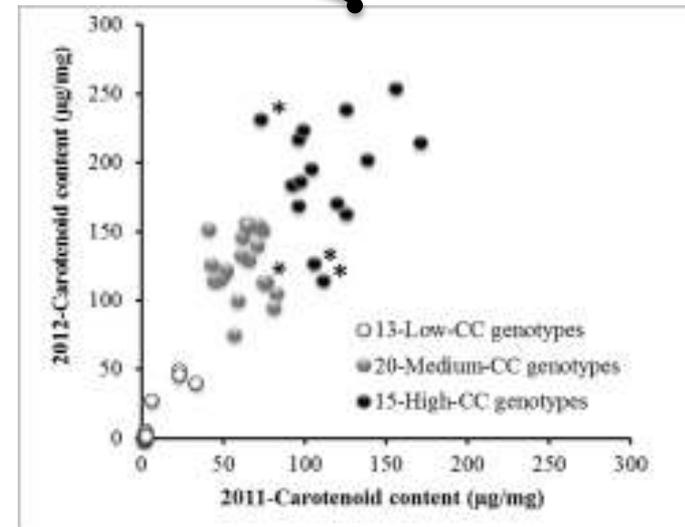


illumina®

2x101 paired-end



Target: 34 geni di pomodoro appartenenti alla via metabolica dei carotenoidi (MEP)



48 genotipi che differiscono per il contenuto di carotenoidi (*cis*-, *trans*-lycopene and β -carotene)

ARRICCHIMENTO E CATTURA DI REGIONI BERSAGLIO (II)

GBS (Genotyping-By-Sequencing): fa uso del potere discriminatorio di enzimi in gardo di tagliare la molecola di DNA (endonucleasi di restrizione) per produrre frammenti di restrizione tra individui in una popolazione.

Taranto et al. BMC Genomics (2018) 17:943
DOI 10.1186/s12864-016-3297-7

BMC Genomics

SCIENTIFIC REPORTS

RESEARCH ARTICLE

Open Access



OPEN GBS-derived SNP catalogue unveiled wide genetic variability and geographical relationships of Italian olive cultivars

Received: 23 October 2017
Accepted: 17 October 2018
Published online: 25 October 2018

Nunzio D'Agostino¹, Francesco Taranto¹, Salvatore Compagno¹, Giacomo Mangini², Valentina Fanelli¹, Susanna Giubletta¹, Monica Marianna Miazzi¹, Stefano Pavan¹, Valentina di Rienzo¹, Wilma Gabrini¹, Luca Lombardo¹, Saverio Zaccaro¹, Oreste Ferrò¹, Concetta Lotti¹, Elena Clari¹ & Cinzia Montemurro¹

Genome-wide SNP discovery and population structure analysis in pepper (*Capsicum annuum*) using genotyping by sequencing

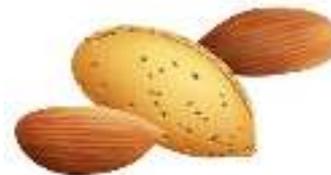
F. Taranto, N. D'Agostino, B. Greco, T. Cardi and P. Tripodi[✉]

THE PLANT GENOME ■ JULY 2017 ■ VOL. 10, NO. 2

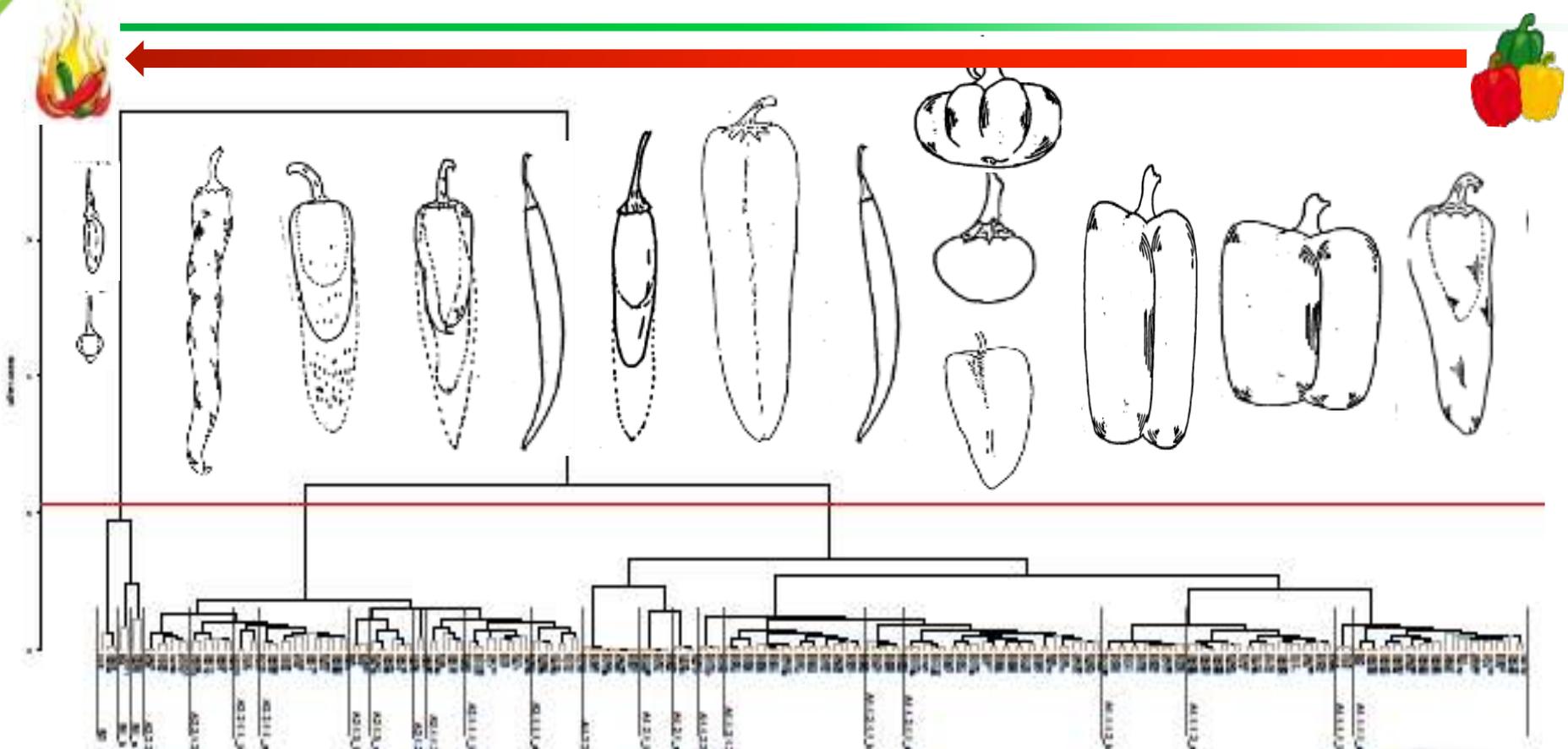
ORIGINAL RESEARCH

A Distinct Genetic Cluster in Cultivated Chickpea as Revealed by Genome-wide Marker Discovery and Genotyping

Stefano Pavan,^{*} Concetta Lotti, Angelo R. Marcotrigiano, Rosa Mazzeo, Nicoletta Bardaro, Valentina Bracuto, Francesca Ricciardi, Francesco Taranto, Nunzio D'Agostino, Adalgisa Schiavulli, Claudio De Giovanni, Cinzia Montemurro, Gabriella Sonnante, and Luigi Ricciardi



STUDIO DELLA DIVERSITÀ GENETICA

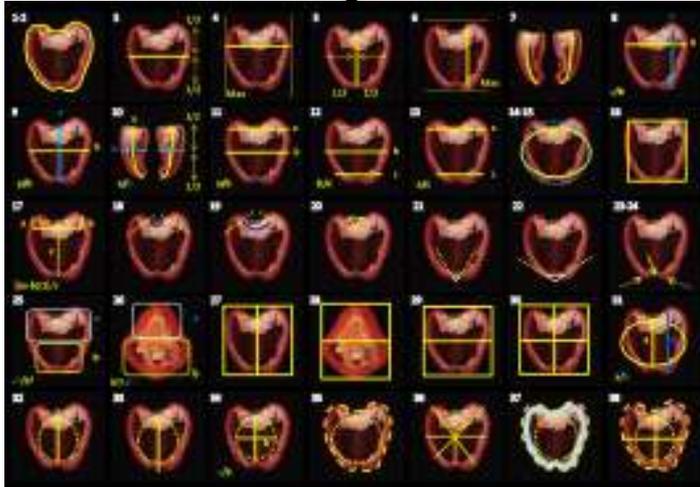


- Ornam
- Asiatici
- Americhe
- Europa
- Calabresi
- Sud Italia
- Nord italia dolci
- Est Europa



LEGARE L'INFORMAZIONE CODIFICATA NEL DNA AI CARATTERI OSSERVABILI

37 caratteri legati alla morfologia del frutto



~4.5K fruits
~9K sections scanned
~330K data points

746k SNPs

	G	C	A	T	C	G	T
	G	C	A	A	C	G	T
	G	C	A	T	T	G	T
	G	G	A	T	C	C	T

Struttura della popolazione
Q matrix

220 accessioni

K7

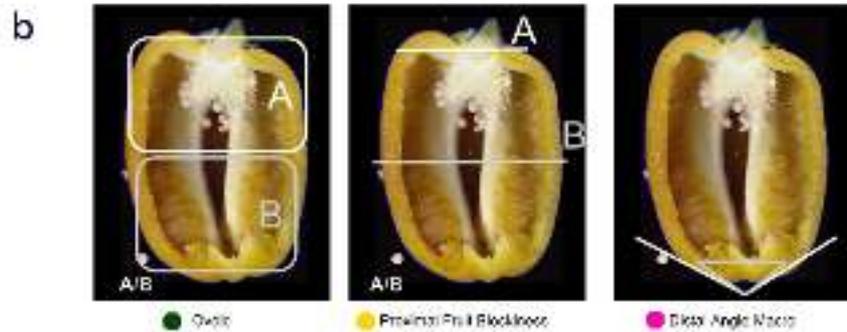
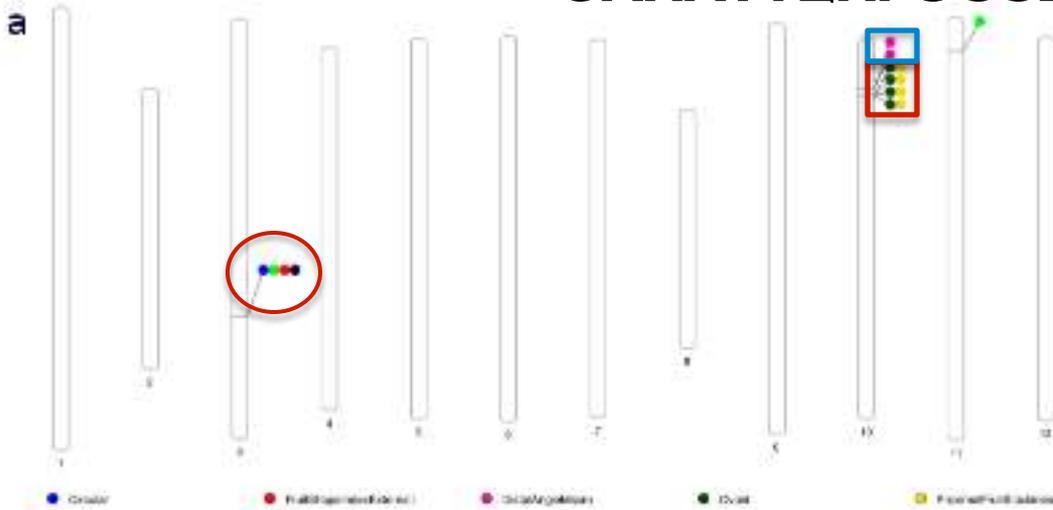


membership coefficient $q > 0.6$

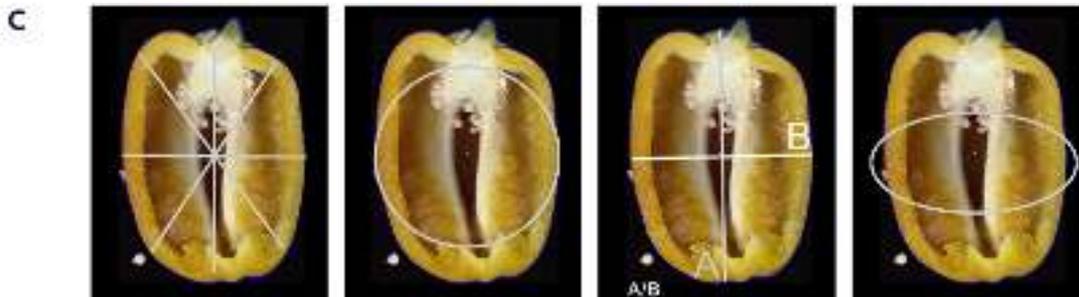
GWAS

mixed linear model (MLM)

LEGARE L'INFORMAZIONE CODIFICATA NEL DNA AI CARATTERI OSSERVABILI



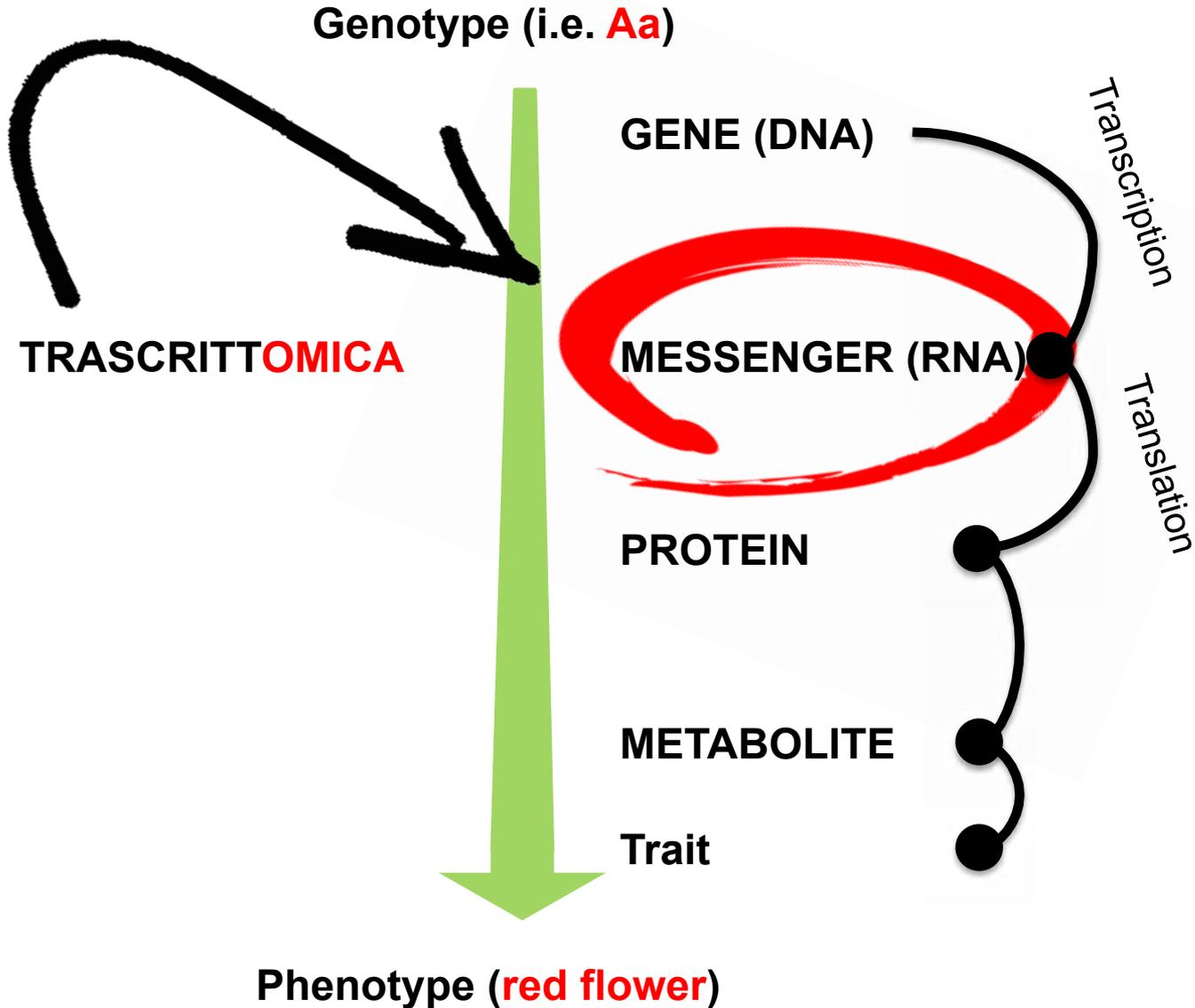
Appuntito o quadrato?



Circolare o allungato ?



IL DOGMA CENTRALE DELLA BIOLOGIA MOLECOLARE





ARRICCHIMENTO BASATO SUL TRASCRITTOMA (RNA-SEQ)

 **Combining transcriptomics and metabolomics to investigate ripening and post-harvest fruit withering in a cherry-like tomato landrace**

[Mennella & Parisi CREA-OF]

 **Transcriptome profiling to elucidate *Trichoderma*- and *Pseudomonas fluorescens*-tomato plant cross-talk.**

[Tucci CNR-IBBR, Lorito UniNA-DiA] & [Zaccardelli CREA-OF]

 **Comprehensive transcriptional profiling of NaCl-stressed pepper plants and evaluation of the effects of salt stress on fruit quality**

[Grillo CNR-IBBR & Venezia CREA-OF]

 **Transcriptional reprogramming of zucchini plant during aphid infestation**

[Rao, Corrado & Pennacchio, Digilio UniNa-DiA]

 **RNA-Seq for sustainable soil management in tomato**

[Zaccardelli CREA-OF]



ARTICLE

Open Access

Transcriptome reprogramming, epigenetic modifications and alternative splicing orchestrate the tomato root response to the beneficial fungus *Trichoderma harzianum*

Monica De Palma¹, Maria Salzano¹, Clizia Vilano², Riccardo Aversano², Matteo Lonto², Michela Ruocco², Teresa D'Amico³, Anna Lisa Piccinelli⁴, Nunzio D'Agostino⁵ and Marina Tucci⁶



Data Descriptor

De Novo Transcriptome Assembly of *Cucurbita Pepo* L. Leaf Tissue Infested by *Aphis Gossypii*

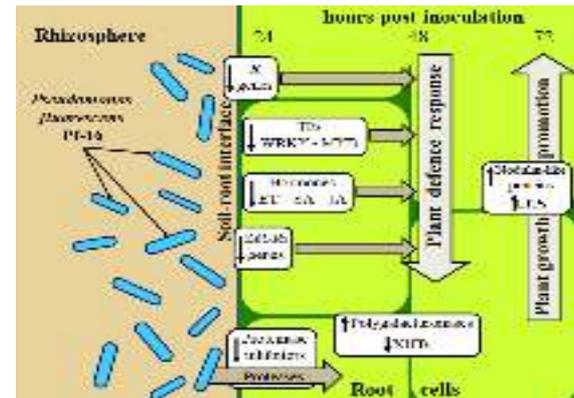
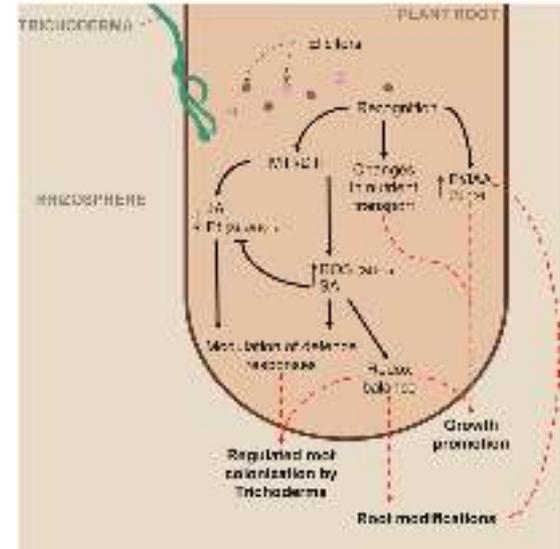
Alessia Vitiello¹, Rosa Rao¹, Giandomenico Corrado¹, Pasquale Chiaiese¹, Maria Cristina Digilio¹, Riccardo Aiese Cigliano² and Nunzio D'Agostino^{3,4}

Symbiosis

DOI : 10.1007/s13199-019-00611-9

Gene expression profiling of tomato roots interacting with *Pseudomonas fluorescens* unravels the molecular reprogramming that occurs during the early phases of colonization

Scotti Riccardo, Nunzio D'Agostino, Massimo Zaccardelli.





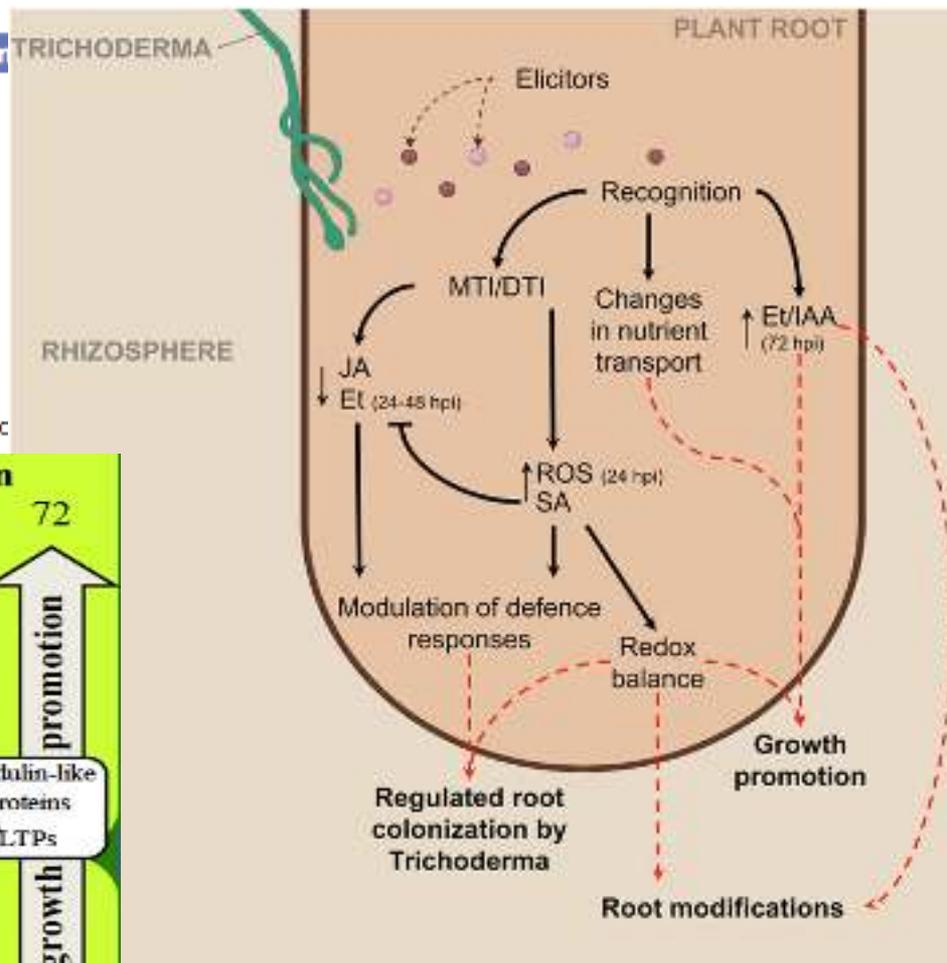
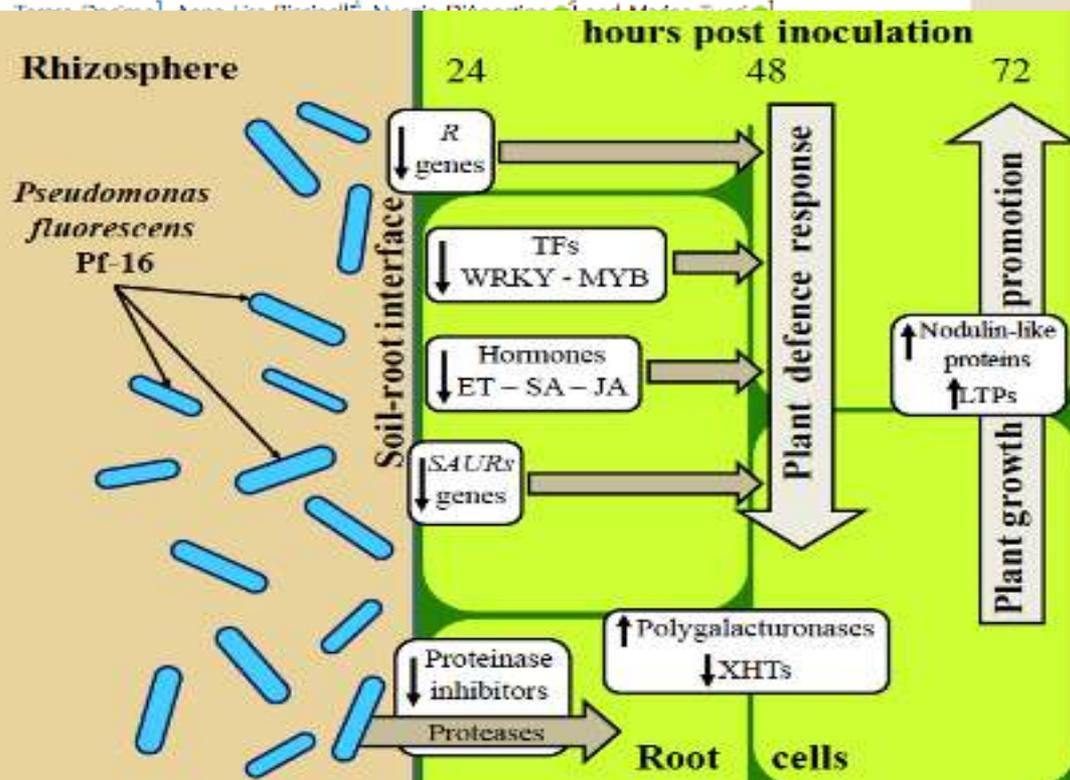
ARRICCHIMENTO BASATO SUL TRASCRITTOMA (RNA-SEQ)

ARTICLE

Open

Transcriptome reprogramming, epigenetic modifications and alternative splicing orchestrate the tomato root response to the beneficial fungus *Trichoderma harzianum*

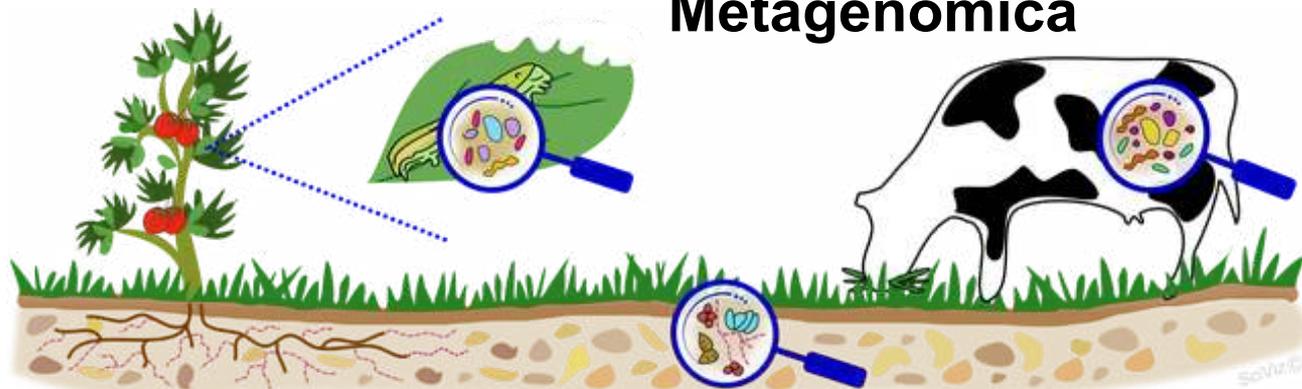
Monica De Palma¹, Maria Salzano¹, Clizia Vilano², Riccardo Aversano², Matteo Lorto², Michela Ruocco²





ULTERIORI SPAZI DI COLLABORAZIONE

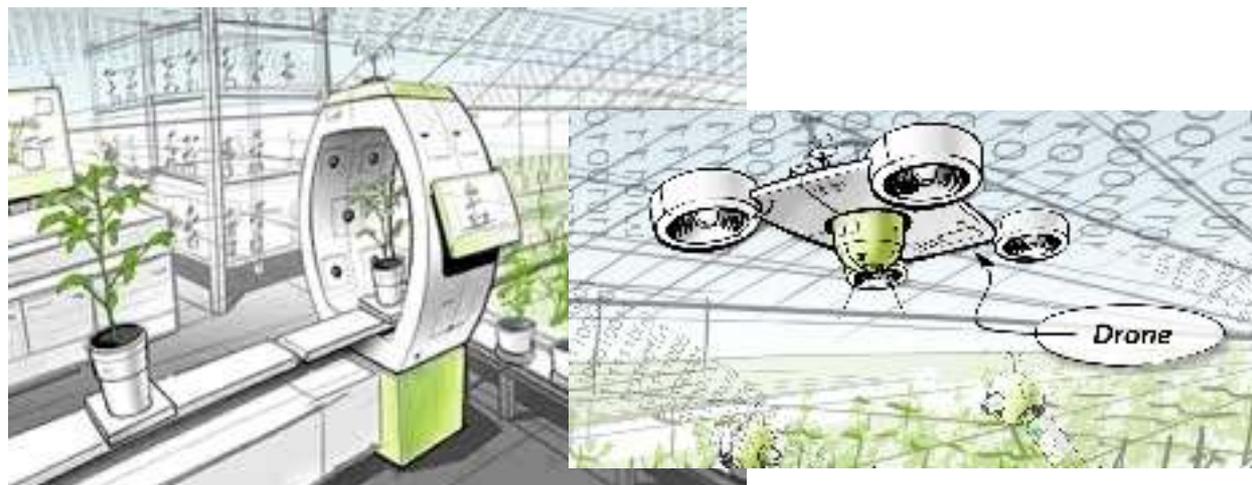
Metagenomica



Genome editing

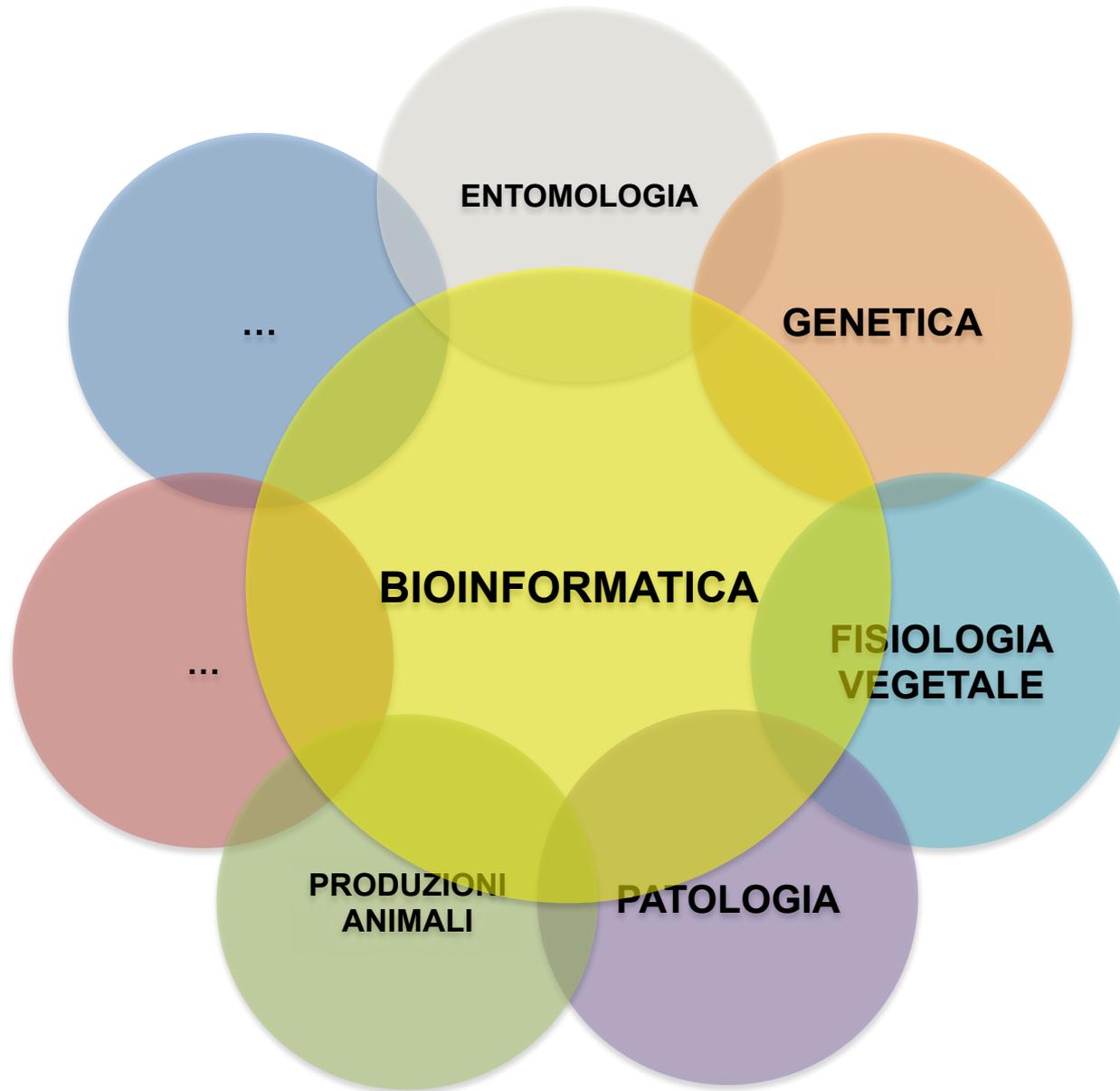
CRISPR-Cas for Fungal Genome Editing: A New Tool for the Management of Plant Diseases

HTPP high throughput plant phenotyping





LA BIOINFORMATICA AL DIA





RINGRAZIAMENTI



Consiglio Nazionale
delle Ricerche



Radboud University

