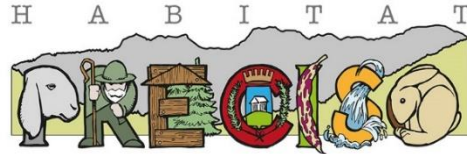


**Il Fagiolo di Lamon  
e il Progetto Habitat:  
un ponte tra altre attività**



FONDAZIONE  
Cariverona

**UNIVERSITÀ  
DEGLI STUDI  
DI UDINE**  
hic sunt futura



# RISULTATI DEL SEQUENZIAMENTO DEL DNA NELLE CINQUE VARIETÀ DI FAGIOLO DI LAMON

**Emanuele De Paoli**  
Docente di Genetica Agraria

Dipartimento di Scienze Agroalimentari, Ambientali e Animali (DI4A)



Spagnolit  
(e Spagnolit Nano)



Spagnol



Calonega



Canalino



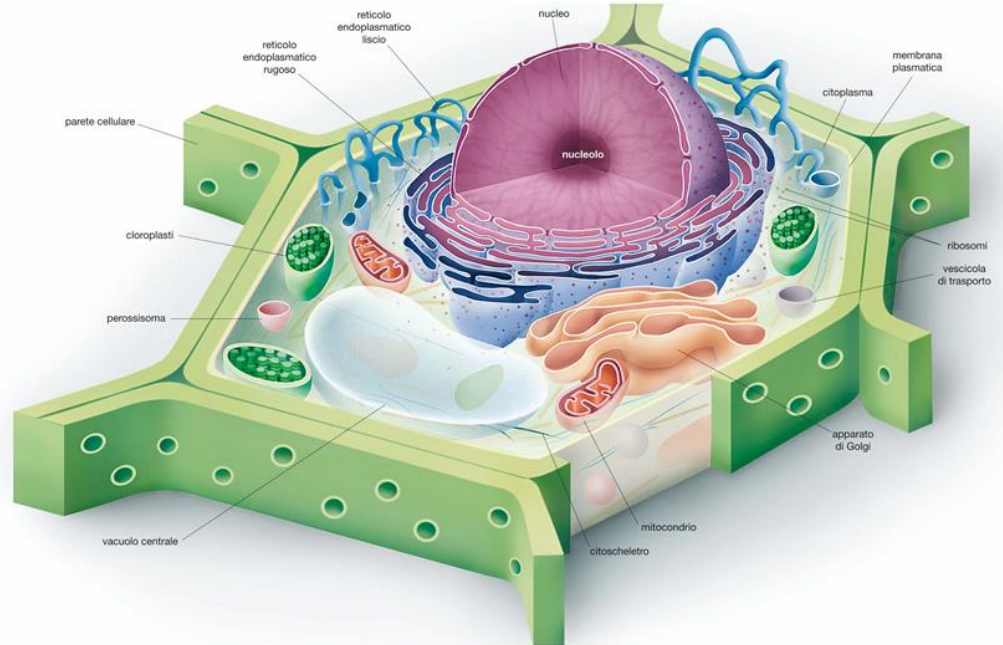
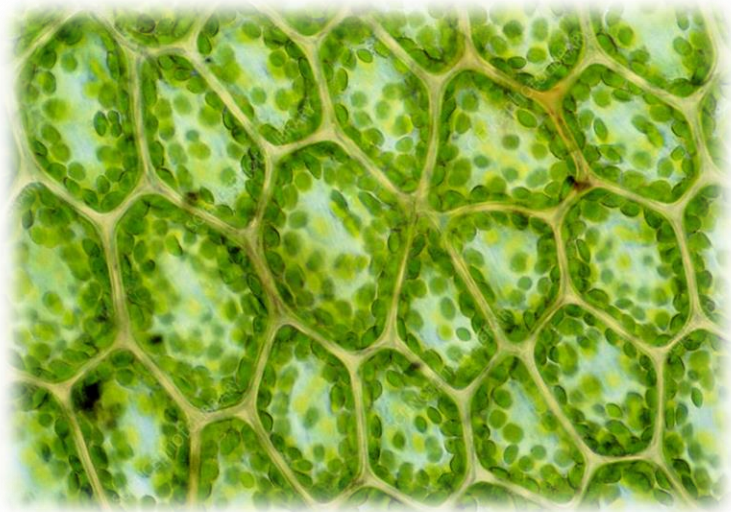
**Possiamo favorire**

- l'identificazione
- la protezione
- la promozione
- il futuro

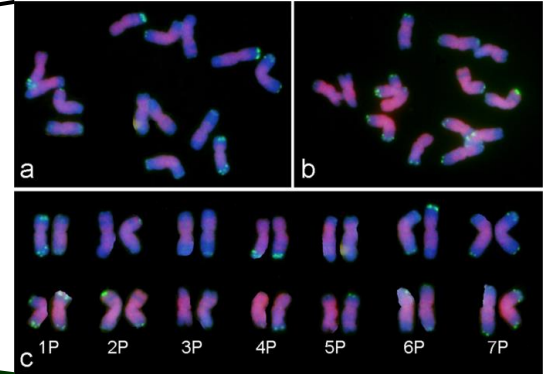
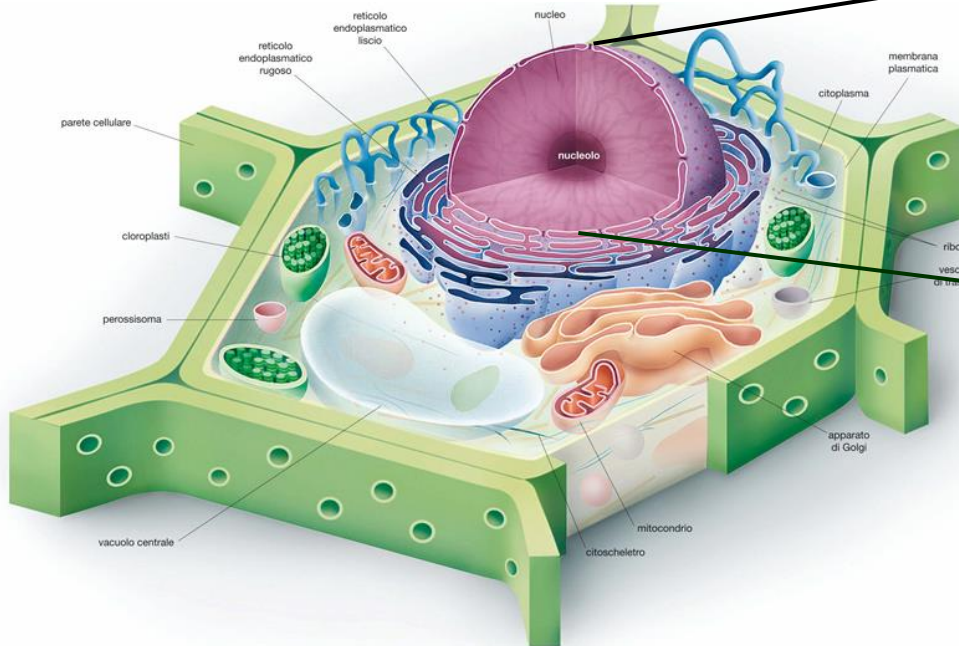
**del fagiolo di Lamon  
mediante le tecnologie del DNA?**



# LA CELLULA VEGETALE

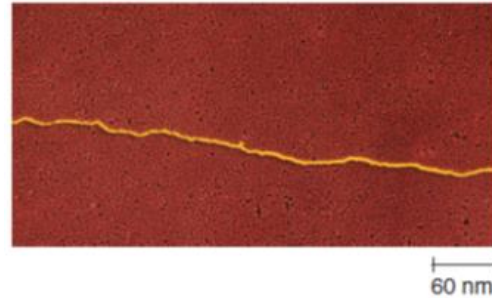
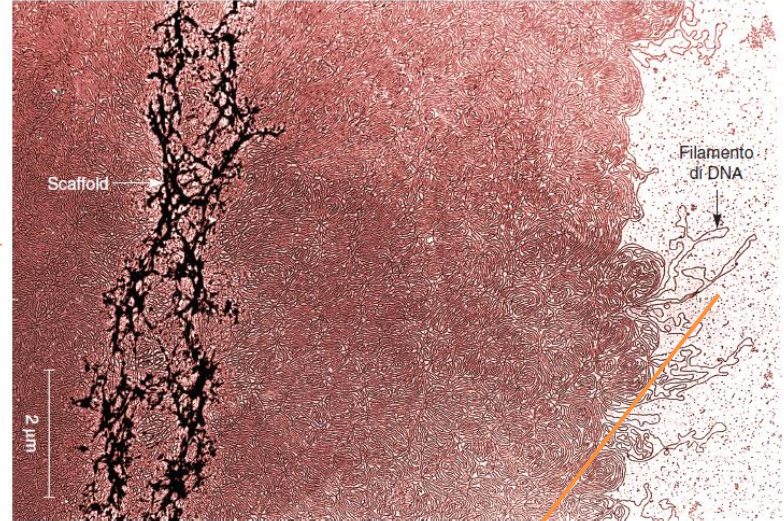
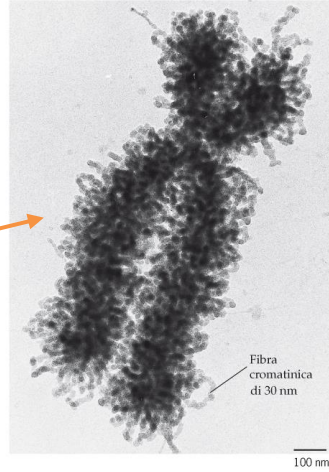
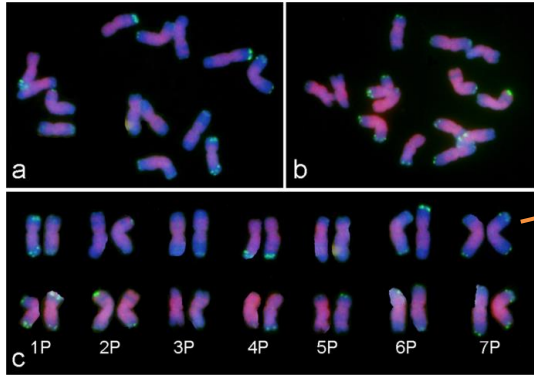


# I CROMOSOMI



**Cromosomi isolati dal  
cereale *Agropyron***

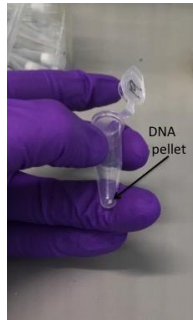
# I CROMOSOMI SONO FATTI DI DNA



# ESEMPIO DI DNA ESTRATTO DALLE CELLULE

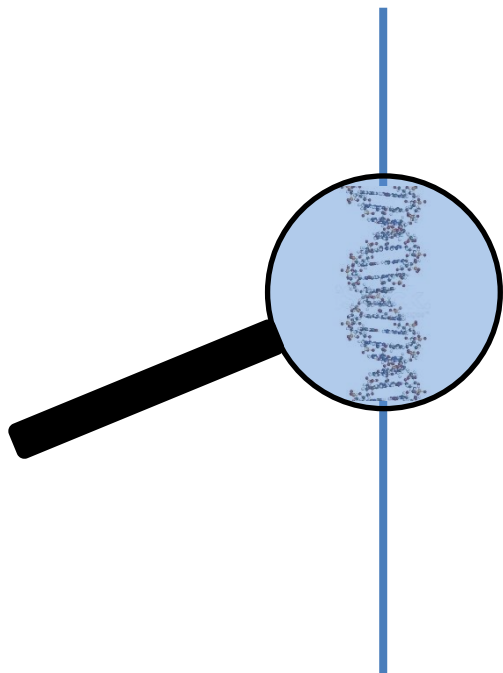


Immagini tratte da youtube (utente: NileRed)



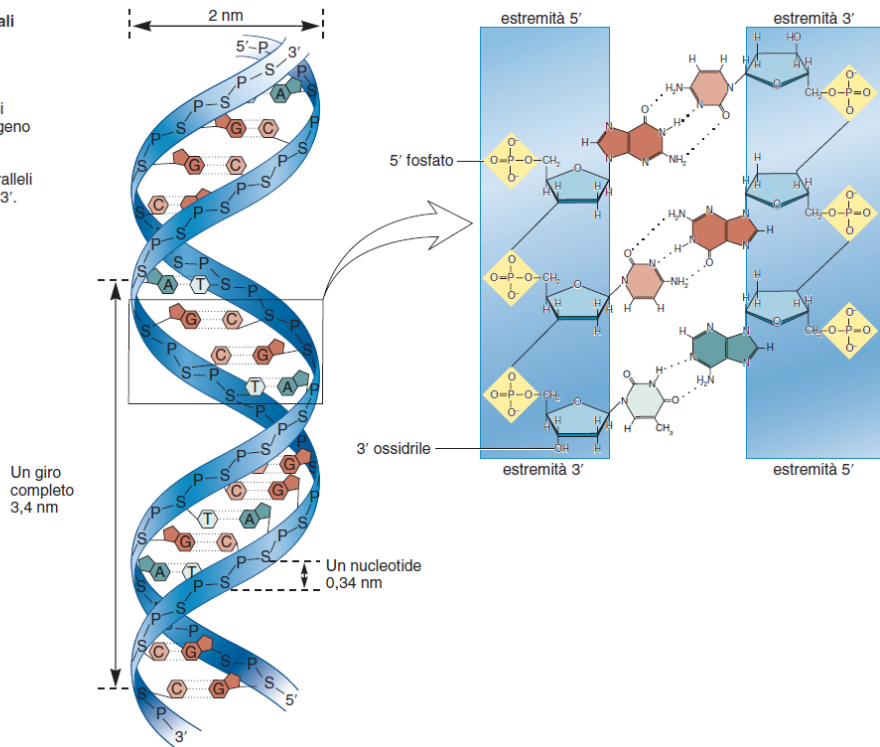
**DNA estratto in laboratorio**

# LA DOPPIA ELICA DEL DNA



## Caratteristiche fondamentali

- I due filamenti formano una doppia elica destrorsa.
- Nei filamenti opposti le basi sono legate da legami idrogeno secondo la regola AT/GC.
- I due filamenti sono antiparalleli rispetto all'orientamento 5'-3'.
- Ci sono circa 10 nucleotidi per giro completo del filamento (360°).



# L'informazione genetica nel DNA



CROMOSOMI



DNA

Sequenziamento  
del DNA



```
GTCCGCCTAGCGACTGCGTGTACGACGTTACGACTACTGCATGCACGCGTACTAGCTAGCATCG  
ACAGTCATCGACTCGCCTCTCCGGTATAFATAGCCCTCTCTCTCTTTTTTATATAAGAGCT  
TCGTCTGGGCTATCAATCGCATACTGATCGTTGTACGCCATGCAACGCTGCATTGATGAAAA  
ATCAGACTGCTACGTACGACGATCGATTCTCTGACATGTGAATATGGTCCGCGCCTATGCTA  
CCCGCATATACGTATCGACATGCTCTGCGCCGGATATAATATCCAAGACTCTGCTGACATAACG  
ATATACTACGATGACCGATGATGTAGACTAGCTACAGACGCACTGAAAGCCGCGCTCTATACG  
ATCTATATCTGCATGCTACGACACGTCACGCTATATGCTGCTATGCAGCCGTCCTAGCCCAA  
CGCACTGATGACTAACCGCTACTGCGCTACTGACTCACTATGCCGCCCGCGCGTGGGGATA  
TACGCTGATCGTACGCGCGCATATCGCGGATCTGCGCTCATTCGCATCGCTATCTACGCATA  
TACCAGATCATGCCGTAATACTACTATGATTATAATCGCTACAGCTAAAAGCTCGATCAATC  
GATAAGACTTATTACGAAAGCGCGTAATATCGTAGCAAACCTATGATTAGCAGGGTCCGATAT  
ACGATCAATGAATGATACTAATTATAACFAATACTCGCGATATCGCGATCCGCGCTACAGTTA  
CGCCACGTATCTATATCGACGCGATATTTTCGATACGAGAAAGTCACTAGCCGCTATCGGGATT  
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GCTACGTACGACAGCTATCTATCTAGCTAGCTACGCTCTATGCTACTGCTACTGCGTTTTACTA  
ACTGCGTACACGACTGACATACTACTCATTACTGACTACTGACTGAATGCCGCGCTAAAGCT  
CTGACGATATGATATGATTTGAATTTGGGGGTGATCATGATGATATGAAATATGACTACTGA  
ACAAATCGATCGATCGACTGACTAGCTAGCTAGCATGACGCGCTAGCGATCGCATGCCGATA  
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GCACTACGCTCACTGCTATTTTCATGCTGACTGCTATGCTATGCTATGATGATGATGATGCA  
TACGCTGACTGCGTACTGACAAAGGTGCATGCCCACTGACTGACTGATGATGAGAGGGGA  
TCGATTGATCGACTGATCGCTGATCGATGCTATTGCACTTTCATACTAAAAGCGCGTCCGATA  
CTGACTGATGAGCTAGCACGTACGGGATCGTGTAGCTAGATATGCTAGCTACGGCGATCGATC  
AATATATCGAGAGTCACTGCGATATATACGCGATAACAGCGGGGCTCTCTCGAGAGAGCTCTT  
ATATACGGCGCGATCAGTCTACTACTCCCACTAGCTACAAAAGATCACTCGCGCCCGGATA
```

SEQUENZIAMENTO DEL DNA

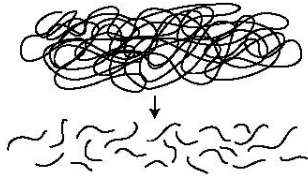




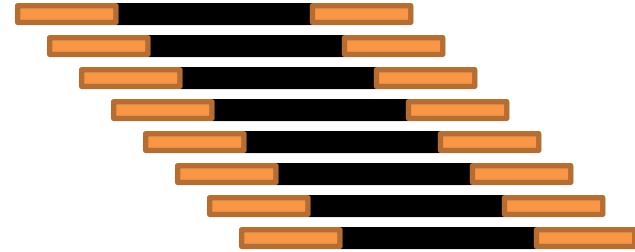
IL FAGIOLO POSSIEDE  
UN GENOMA (DNA)  
LUNGO 587.000.000 DI  
LETTERE

```
GTCCGCTAGCCACTGCCGTGTACGACGTTACGACTACTGCATGACGCCCTACTAGCTAGCATCG  
ACAGTCATCGACTCGCCCTCTGCCCTATATATAGCCCTCTCTCTCTTTTTTATATAGAGAGCT  
TCGTGTGGGTATCAGATCGCATACTGATCGTTGTACCGGATCGAACCTCGCATTGATGAAAA  
ATCAGACTGCTACGTACGACGATCGATTTCTCTGACATGTGAATATGGTCGCGCTATGCTA  
CCCGCATATACGATCGACATGTCTGCGCCCGGATATAAATCCAGACTCTGCTGACATAACG  
ATATACTACGATGACCGATGATGTAGACTAGCTACAGACGCACTGAAAGCGCGCTCTATACG  
ATCTATATCTGCATGCTACGACACGTCACGCTATATGCTGCTATGCAGCCGTCCTAGCCCAA  
CGCACGATGACTAACGCGCTACTGCGCTACTGACTCACTATGCGCGCCGCGCCGTGGGGATA  
TACGCTGATCGTACGCGCGCATATCGGGATCTGCGCTCATATCGCATCGCTATCTACGCATA  
TACCAATCATGCCGTAATAGTACTATGATTATAAATCGCTACAGCTAAAAGCTCGATCAATC  
GATAAGACTTATACGAAAGCGCGTAATATCGTAGCAAACCTATGATTAGCAGGGTCGATAT  
ACGATCAATGAATGATACTAATTATAACTAATACTCGCGATATCGCGATCCGCGCTACAGTTA  
CGCCACGATCTATATCGACCGGATATTTGATACGAGAAAATCAGTAGCGCGCTATCGGGATT  
ACACGTACATATATACCTAAGTACTAATGACTAGCCACTACTGACCTACTAGCTAGCACATT  
TATCATACTGACACTACTCATCACTCAGCAGACATCATTCTAGTGTGTGATGATATGCTATA  
GCTACGTACGACAGTCTATCTACGATCGCTAGCTACGTCGTTATGCTACTCTGCGTTTTACTA  
ACTGCGTACAGCTACTGACATACACTCATTACTGACTACTGACTGAAATGCGCCGCTAATGCT  
CTGACGATATGATATGATTTGAAATTTGGGGTGTATCATGATGATATGAAATATGACTACTGA  
ACAATCGATCGATCGACGTGACTAGCTAGCTAGCATGACGCCCTAGCGATGCGCATGCCGATA  
GTCCACATGCATGCATCAACTATACCTATCATGATCGTACGCCCGCGCGTTTCGCCGATGATC  
ATGCATGCATGCATACCTACTACTGCATGCATACCTGCATGACGGGGTGCATGATCGATCATCAT  
GCAGTACGTCACTACTGCATTTTCATGCTGACTGCATGCATGACTGCATGCATGATGATGCA  
TACGCTGACTGCTACTGACAAGGTGCATGCCACTGACTACTACTGATGATGAGAGGGGA  
TCGATTGATCGACTGATCGTCTGATCGATGCATTGCACTACTTCTAGATAAAGCGCGCTGCATA  
CTGACTGATGAGCTAGCACGTACGGGATCGTCTAGCTAGATATGCTAGCTACGGCGATCGATC  
AATATATCGAGAGTCACTCGGATATATACCGGATAACAGCGGGGCTCTCTCGAGAGAGCTCTT  
ATATACCGCGCGATCACTCTACTACTCCACTAGCTACAAAGATCACTCGCGCGCGGATA
```

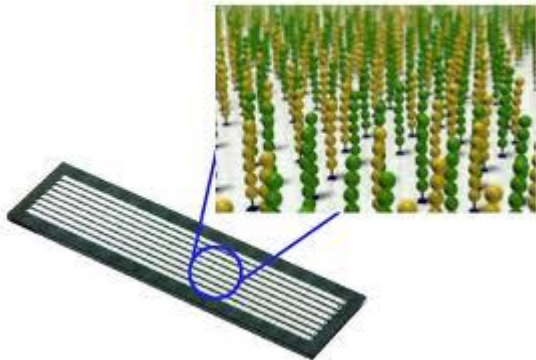
# PREPARAZIONE DEL DNA PER IL SEQUENZIAMENTO



**MISCELA DI FRAMMENTI  
DI DNA DALLA PIANTA**



**LIBRERIA DI FRAMMENTI**



cBOT

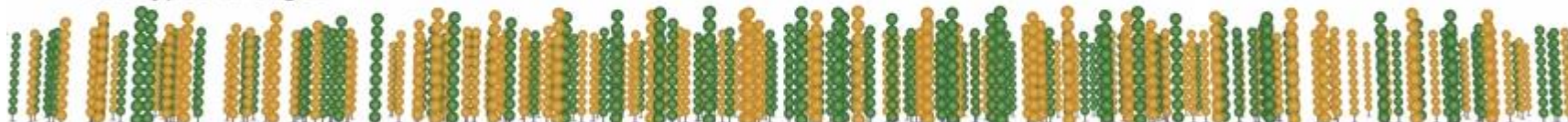
**ADATTATORE  
A MONTE**

**INSERTO DI  
DNA**

**ADATTATORE  
A VALLE**



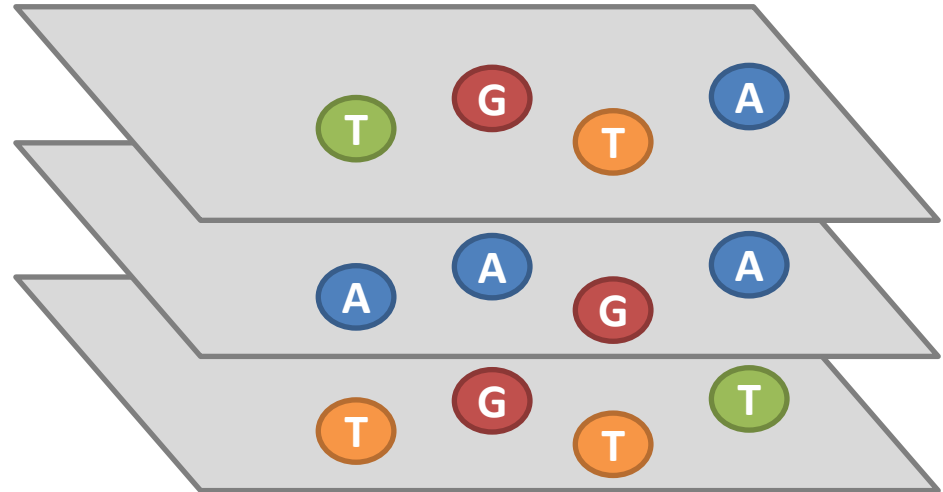
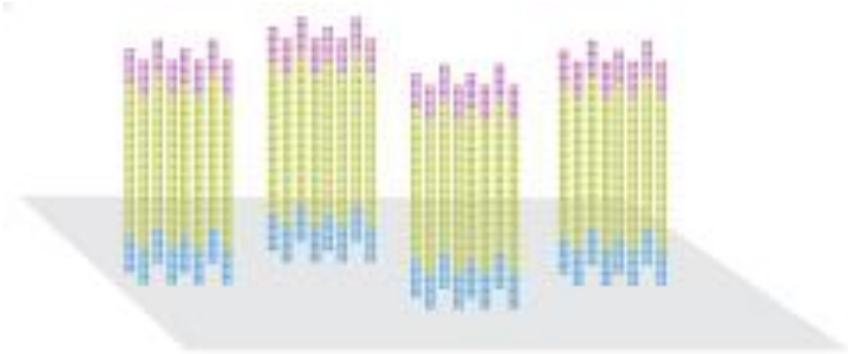
The flowcell contains  
two types of oligos



**OLIGONUCLEOTIDI  
COMPLEMENTARI AGLI  
ADATTATORI A MONTE**

**OLIGONUCLEOTIDI  
COMPLEMENTARI AGLI  
ADATTATORI A VALLE**

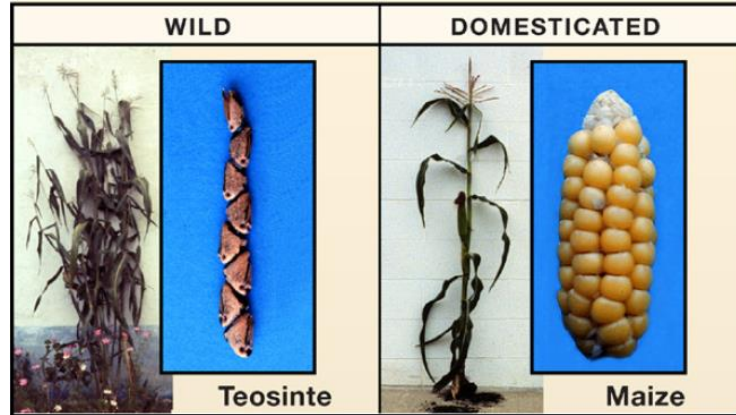
# SEQUENZIAMENTO (LETTURA DELLE BASI-LETTERE DEL DNA)





# UNA DISCENDENZA INSOSPETTIBILE

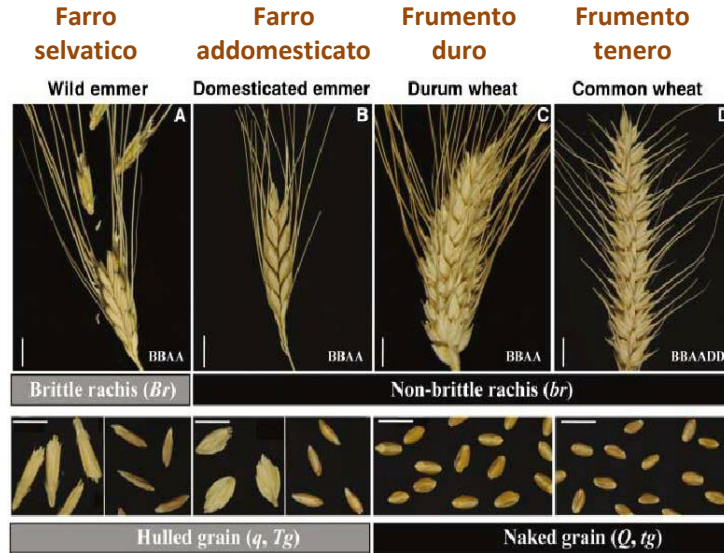
Teosinte  
Progenitore del mais,  
interfertile



Mais  
Prime tracce: 9000-7000 anni fa  
nell'attuale Messico

Solo **cinque regioni genomiche differenti**  
Due di queste ospitano un solo gene ciascuna.  
A questi **due geni** sono riconducibili  
le **principali differenze** tra le due piante

# DUE IMPORTANTI MUTAZIONI A FAVORE DELLA COLTIVAZIONE DEL FRUMENTO



Rachide della spiga fragile



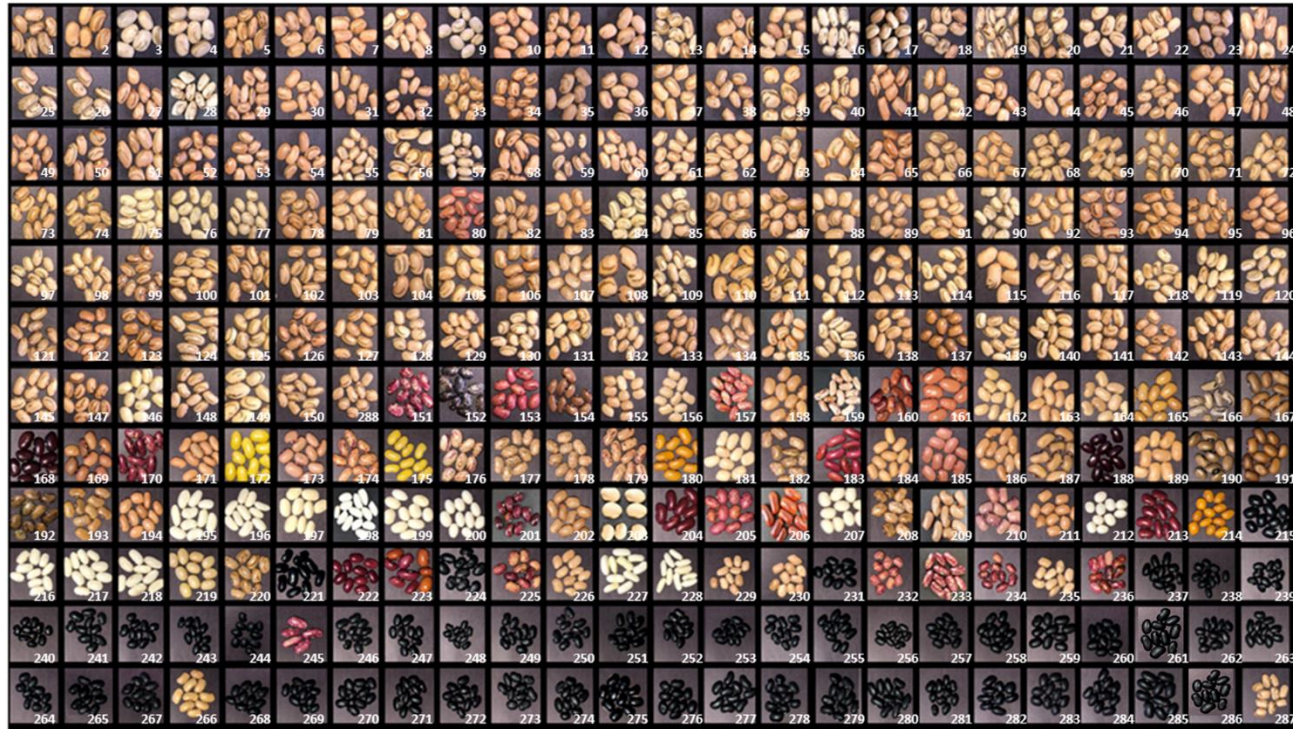
Rachide della spiga resistente

Seme vestito



Seme nudo

# DIVERSITÀ FENOTIPICA DEL SEME DI FAGIOLO



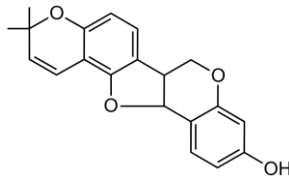
Fonte: de Carvalho Paulino et al. Genetic diversity and inter-gene pool introgression of Mesoamerican Diversity Panel in common beans (Journal of Applied Genetics, 2021)



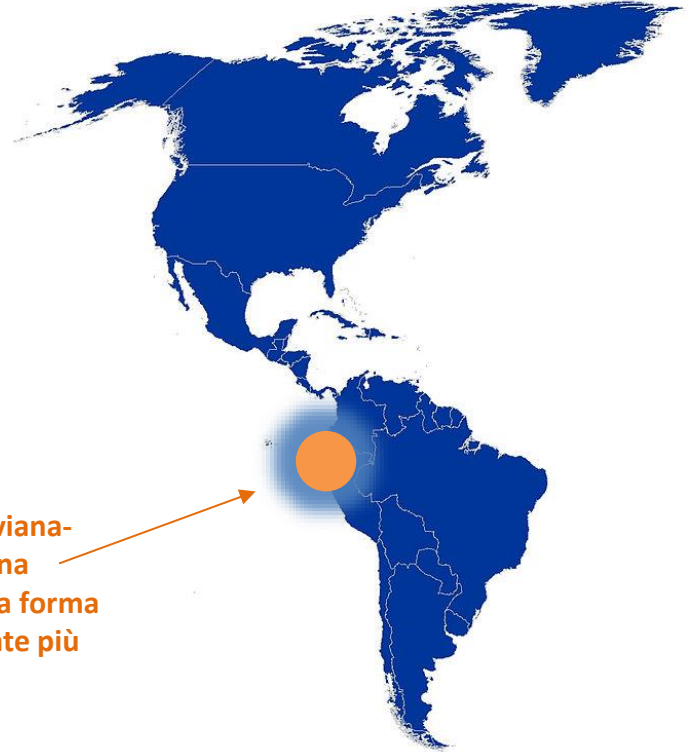
# LA FASEOLINA E LE PRIME IPOTESI (ERRATE) SULL'ORIGINE GEOGRAFICA DEL FAGIOLO



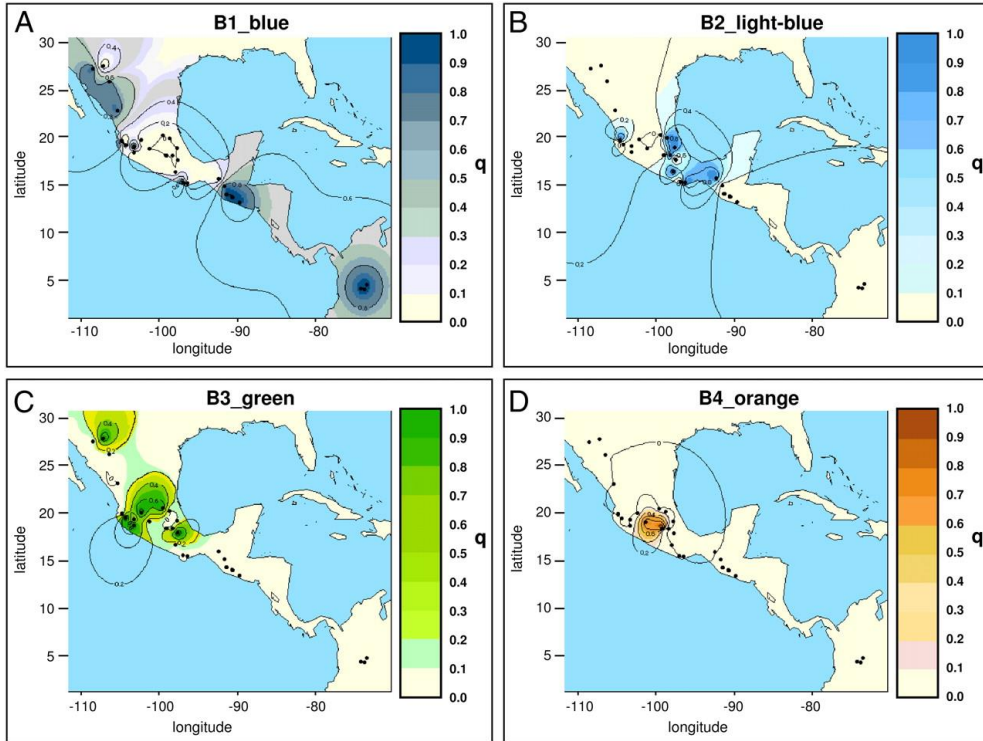
**Faseolina, la principale  
proteina di riserva dei  
semi di fagiolo**



**Regione Peruviana-  
Ecuadoregna  
(Faseolina in una forma  
apparentemente più  
antica)**



# CENTROAMERICA – PUNTO DI ORIGINE DEL FAGIOLO

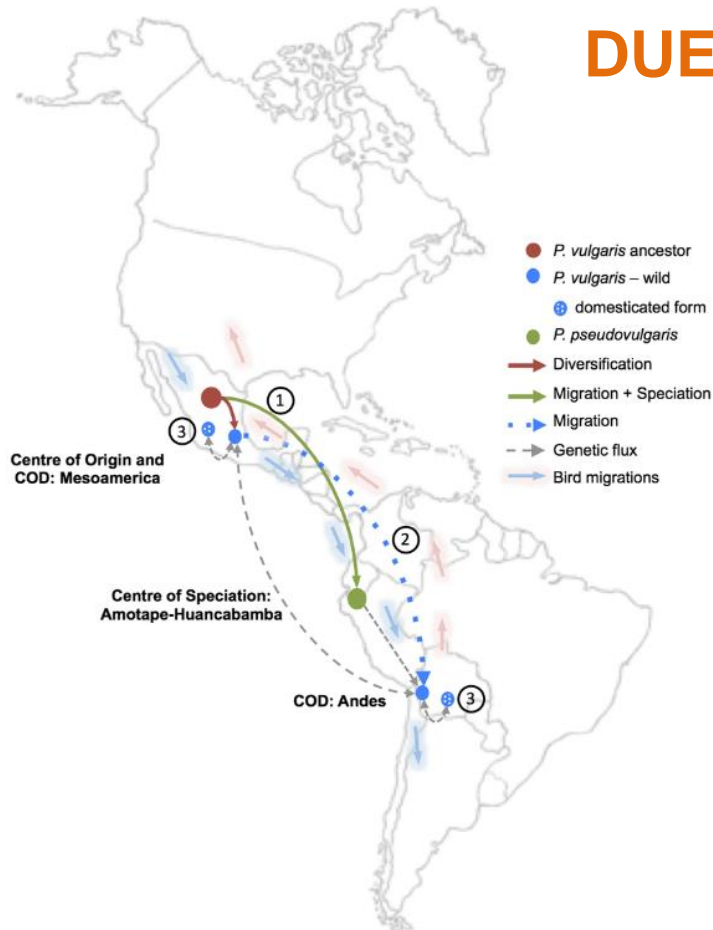


Population genetics statistics for the five gene fragments and the concatenate sequences in the different gene pools of *P. vulgaris*

Population	N	V	Pi	S	H	Hd	$\pi \times 10^{-3}$	$\theta_W \times 10^{-3}$	D
Concatenate									
All	84	137	123	14	56	0.96	9.9	8.3	—
MW	37	119	98	21	34*	0.99*	10.6*	8.7*	—
AW	43	32	22	10	18	0.86	1.0	2.3	—
Phi	4	18	0	18	4	1.00	2.7	3.0	—

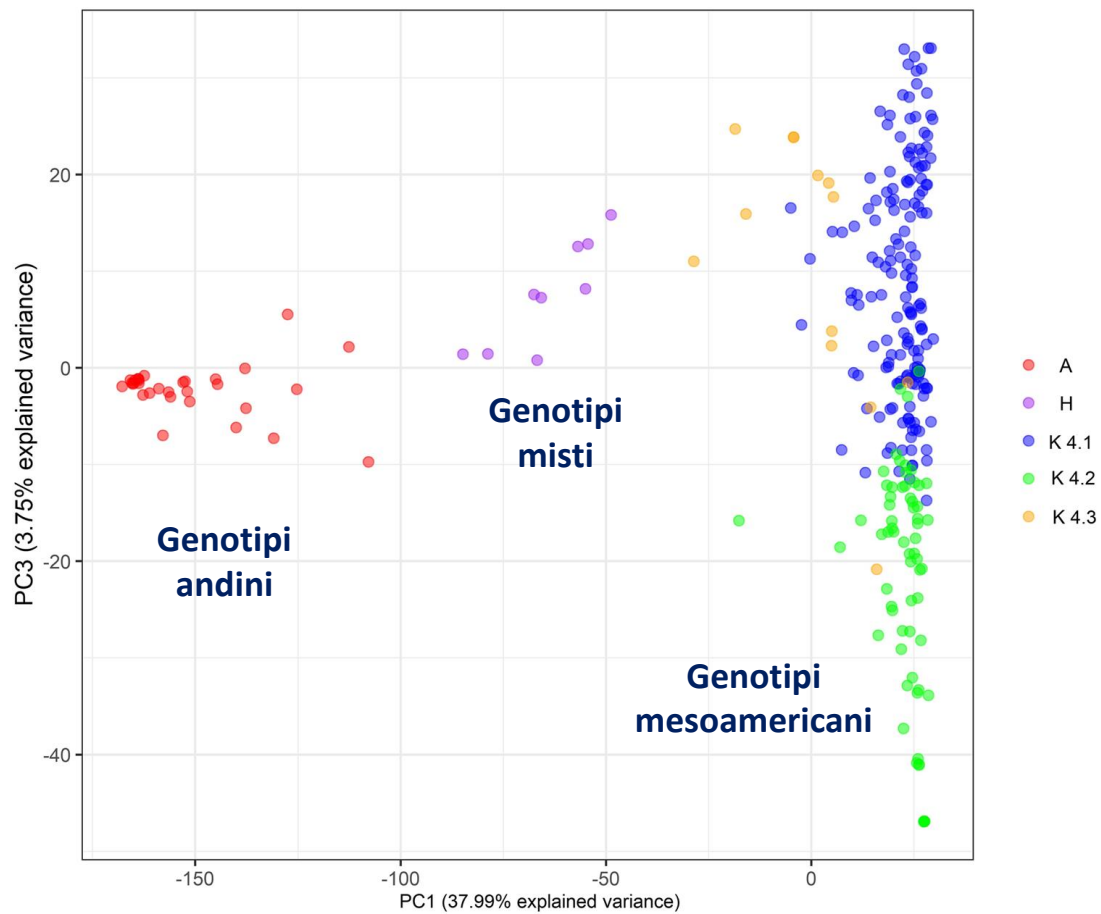
Minore diversità genetica nel gruppo andino

# DUE CENTRI DI ADDOMESTICAMENTO DEL FAGIOLO

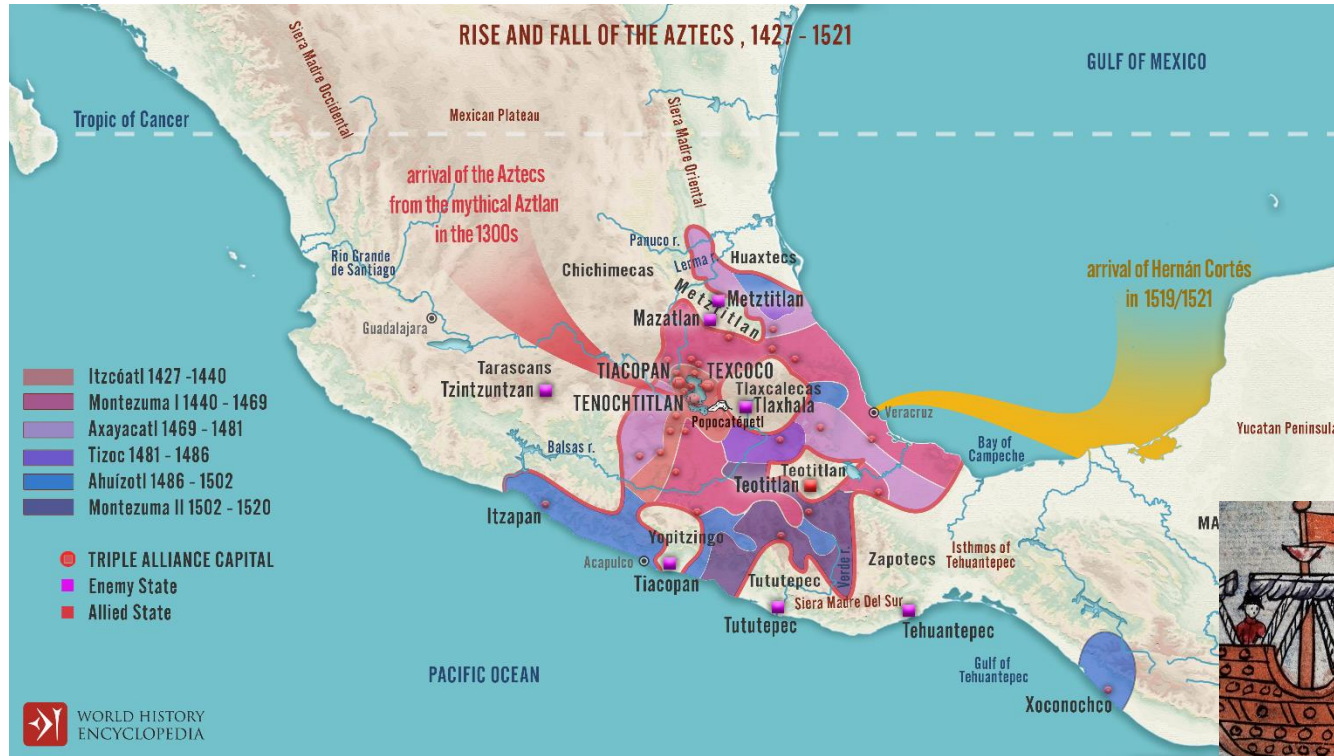


L'addomesticamento del fagiolo è avvenuto  
~8000 anni fa in due contesti ecogeografici  
distinti e contrastanti:

Regione mesoamericana (Messico)  
Regione andina (Sud America)



# LA CONQUISTA DI CORTÉZ IN MESSICO (1521)



# PIETRO VALERIANO

«Secondo la ricostruzione biografica scritta dal Ticozzi nel 1813, Piero Valeriano nella primavera del 1532 aveva partendo di Roma ricevuto da Papa Clemente alcuni semi di varie specie di Smilace perché lo propagasse nel territorio Bellunese, ove giunto in Maggio del 1532, di niuna cosa fu più sollecito che di affidare alla terra questo prezioso arbusto.»



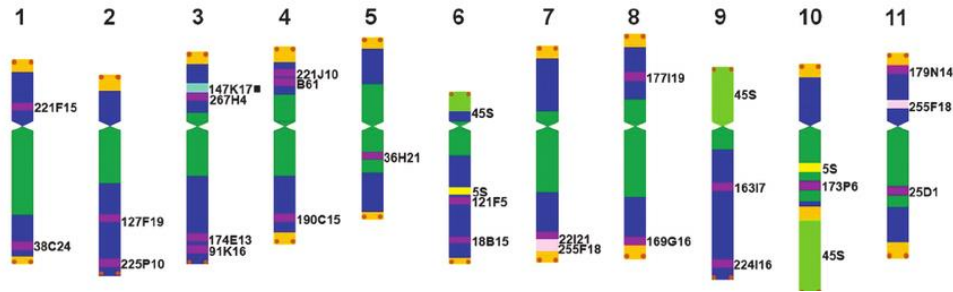
# SEQUENZIAMENTO DEL DNA

<b>1. Calonega</b>	<b>COMPLETATO</b>
<b>2. Canalino</b>	<b>COMPLETATO</b>
<b>3. Spagnolo</b>	<b>COMPLETATO</b>
<b>4. Spagnolet</b>	<b>COMPLETATO</b>
<b>5. Spagnolet Nano</b>	<b>COMPLETATO</b>

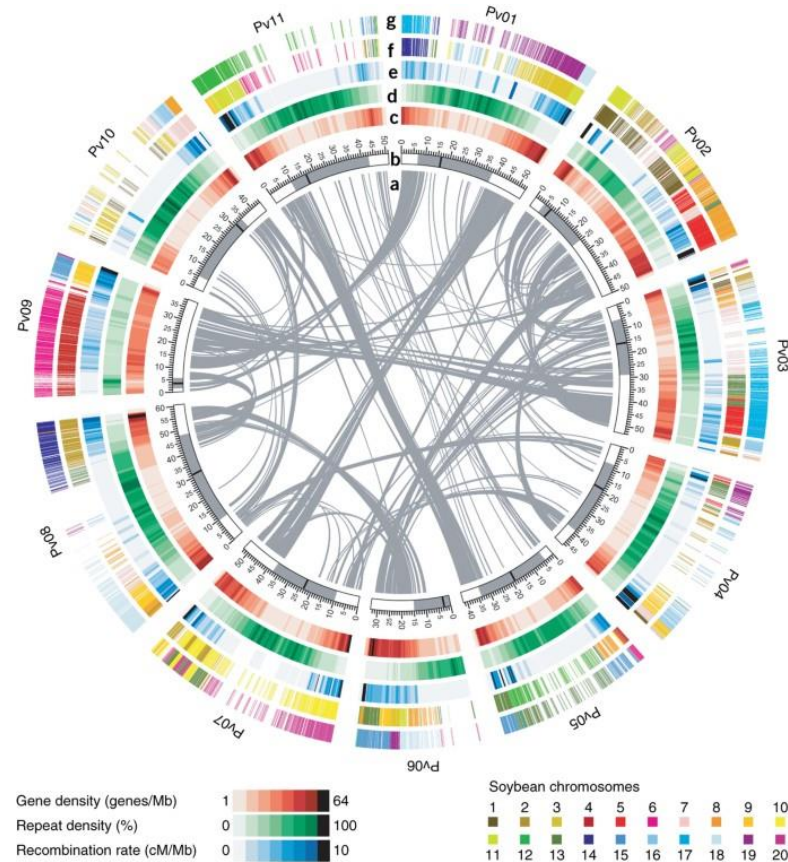
**1700 milioni di sequenze di 150 paia di basi ciascuna con una media di circa 113 milioni di sequenze per varietà, corrispondenti a una copertura di sequenziamento di circa 30 genomi equivalenti per varietà**

# La struttura del genoma del fagiolo (*Phaseolus vulgaris*)

*P. vulgaris* cv. BAT93

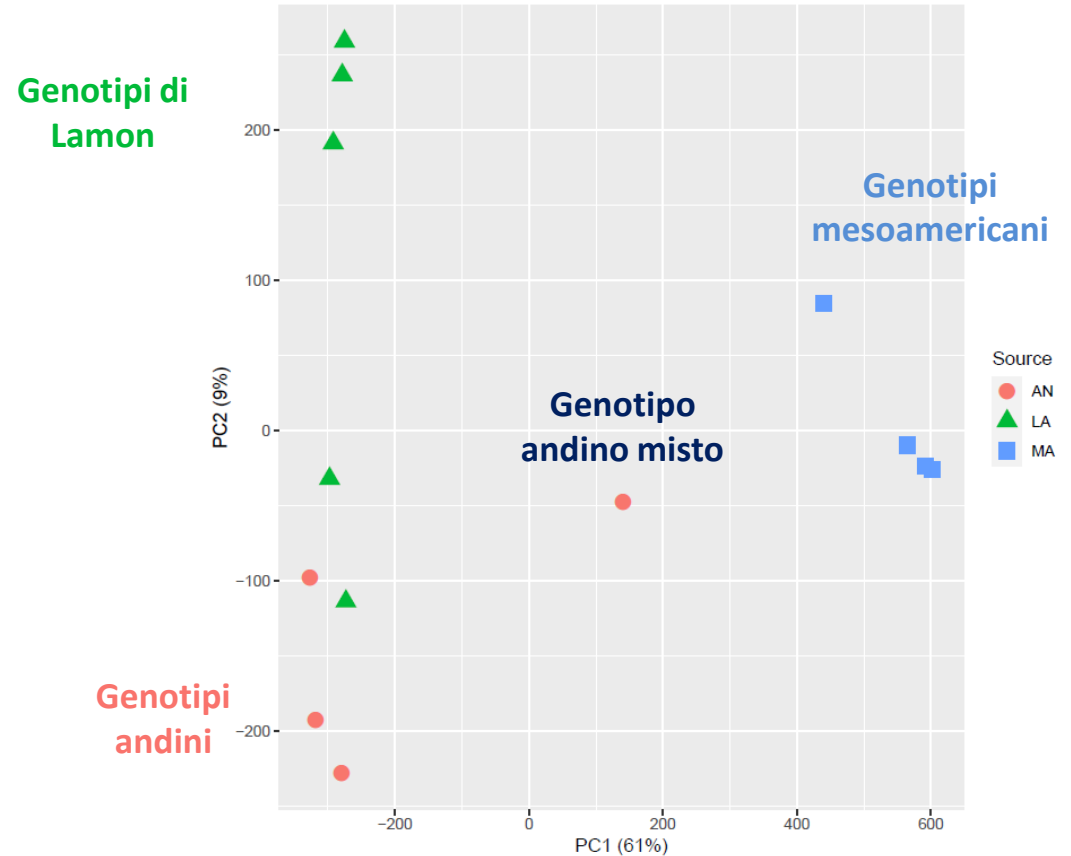


>500.000 polimorfismi  
analizzati





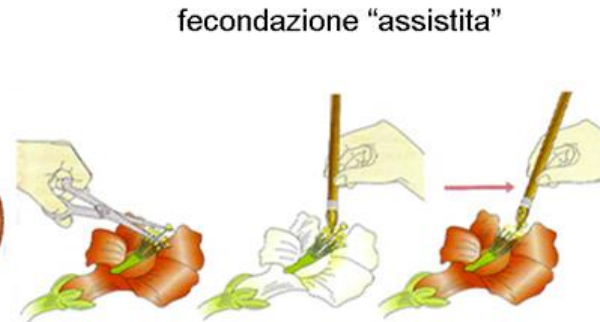
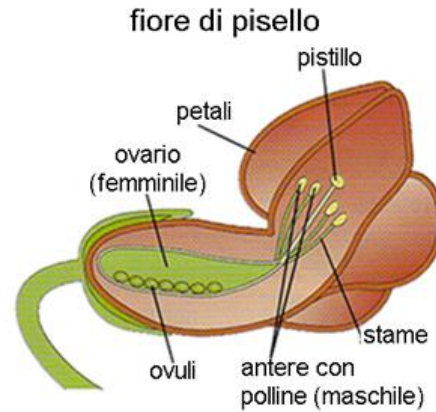
# LA COLLOCAZIONE GENETICA DEL FAGIOLO DI LAMON



# OBIETTIVI PREFISSATI E IN CORSO

- (i) caratterizzare l'**identità genetica** dei fagioli di Lamon.
  - Distinguere i fagioli di Lamon da imitazioni
  - Valutare partner di incrocio adatti
- (ii) valutare l'applicabilità di **sistemi di incrocio ad impollinazione incrociata** alle varietà di fagiolo coltivate a Lamon per la futura identificazione di geni specifici, responsabili di caratteri di interesse.

# PROVE DI FECONDAZIONE INCROCIATA





FONDAZIONE  
*Cariverona*

**NEL DNA DI LAMON**