

WEBINAR VALFRUIT **VALorization of genetic resources to improve FRUIT crops**

Valorizzazione delle risorse genetiche
per il miglioramento della resilienza
dei sistemi frutticoli

Martedì 28 ottobre
Ore 16:30–18:30

Metodologie per la caratterizzazione genetica e fenotipica

Il pangenoma di Arancio Rosso



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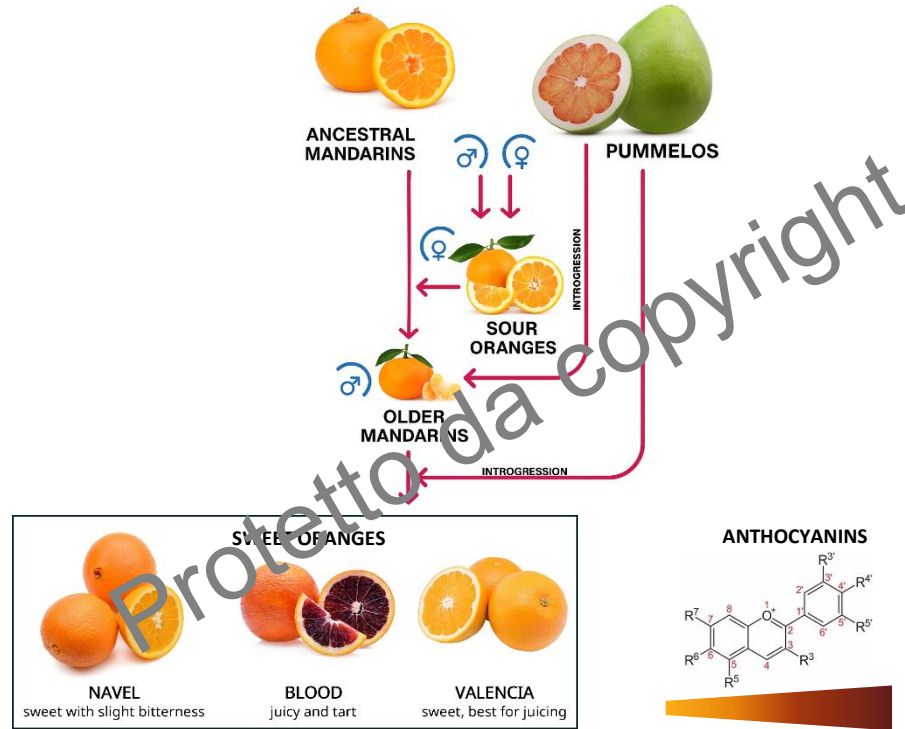


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La storia dell'arancio



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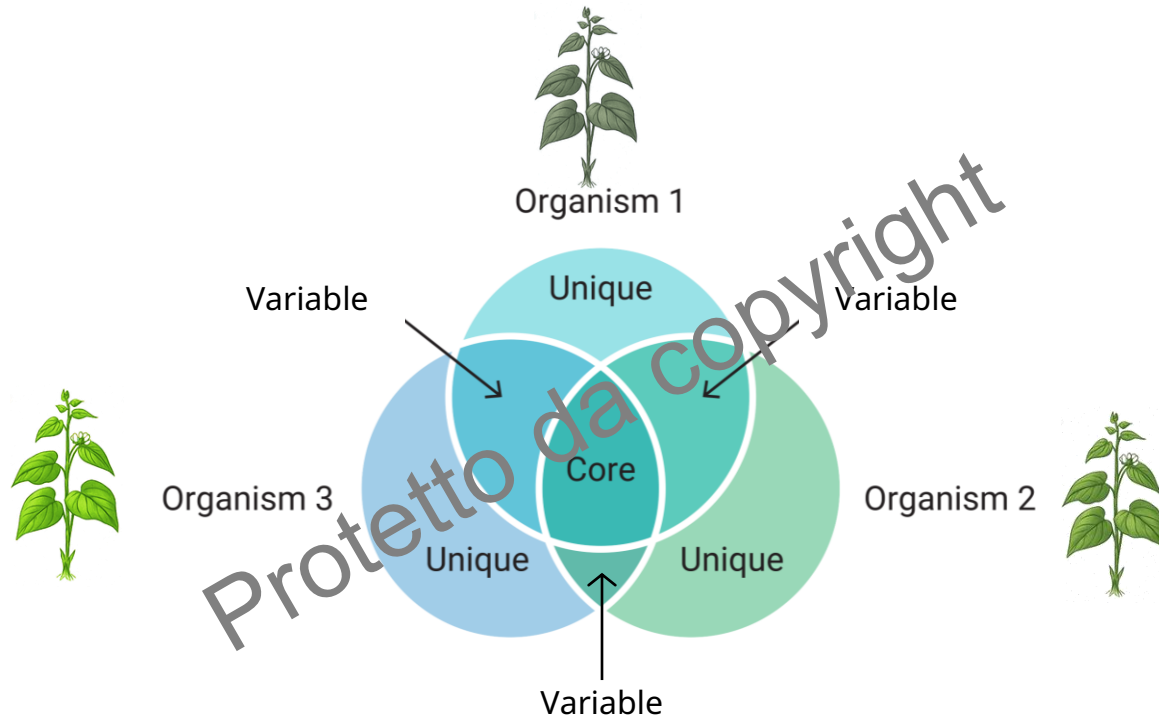


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Diversità genomica di una specie



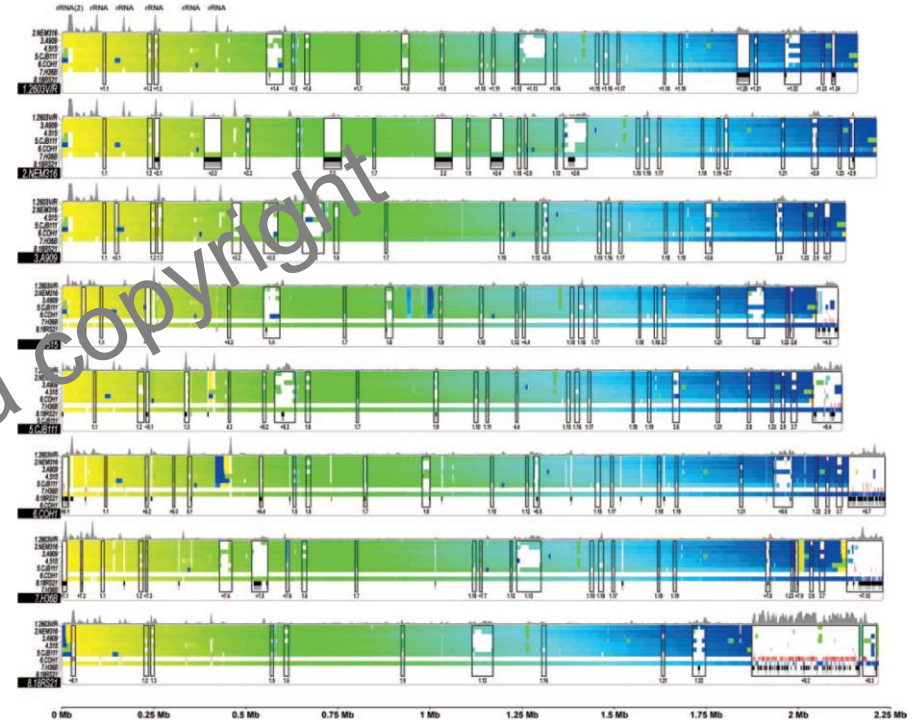
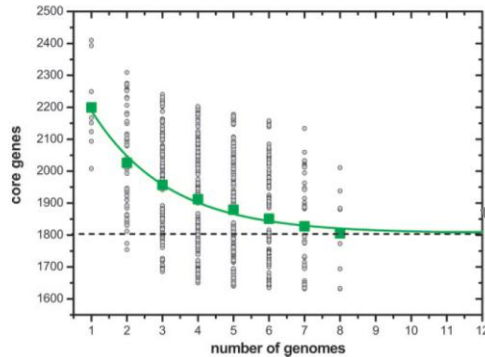
pan-genomi

Genome analysis of multiple pathogenic isolates of *Streptococcus agalactiae*: Implications for the microbial "pan-genome"

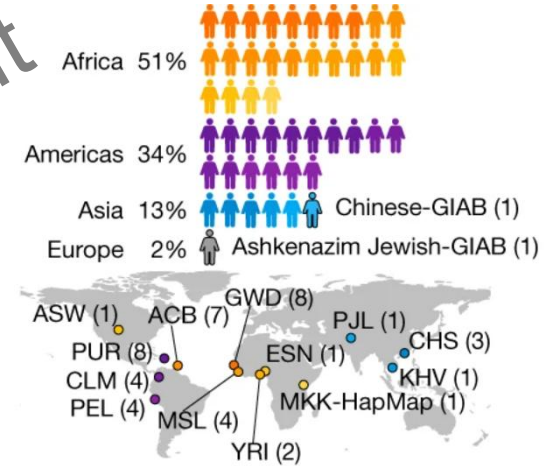
Hervé Tettelin^{a,b}, Vega Masignani^{b,c}, Michael J. Cieslewicz^{b,d,e}, Claudio Donati^c, Duccio Medini^c, Naomi L. Ward^{a,f}, Samuel V. Angiuoli^g, Jonathan Crabtree^h, Amanda L. Jones^g, A. Scott Durkin^g, Robert T. DeBoy^g, Tanja M. Davidsen^g, Mariora Mora^g, Maria Scarselli^c, Immaculada Margarit y Ros^g, Jeremy D. Peterson^g, Christopher R. Hauser^g, Jaideep P. Sundaram^g, William C. Nelson^g, Ramana Madupu^g, Lauren M. Brinkac^g, Robert J. Dodson^g, Mary J. Rosovitz^g, Steven A. Sullivan^g, Sean C. Daugherty^g, Daniel H. Haft^g, Jeremy Selengut^g, Michelle L. Gwinn^g, Liwei Zhou^g, Nikhat Zafar^g, Hoda Khouri^g, Diana Radune^g, George Dimitrov^g, Kisha Watkins^g, Kevin J. B. O'Connor^h, Shannon Smith^h, Teresa R. Utterback^h, Owen White^g, Craig E. Rubens^g, Guido Grandi^c, Lawrence C. Madoff^{h,i}, Dennis L. Kasper^{a,j}, John L. Telford^c, Michael R. Wessels^{d,e}, Rino Rappuoli^{c,k,l}, and Claire M. Fraser^{a,b,k,m}

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Contributed by Rino Rappuoli, August 5, 2005



Il pangenoma umano



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Pangenomi: potenzialità agronomiche

[nature](#) > [nature communications](#) > [articles](#) > [article](#)

Article | [Open access](#) | Published: 07 September 2023

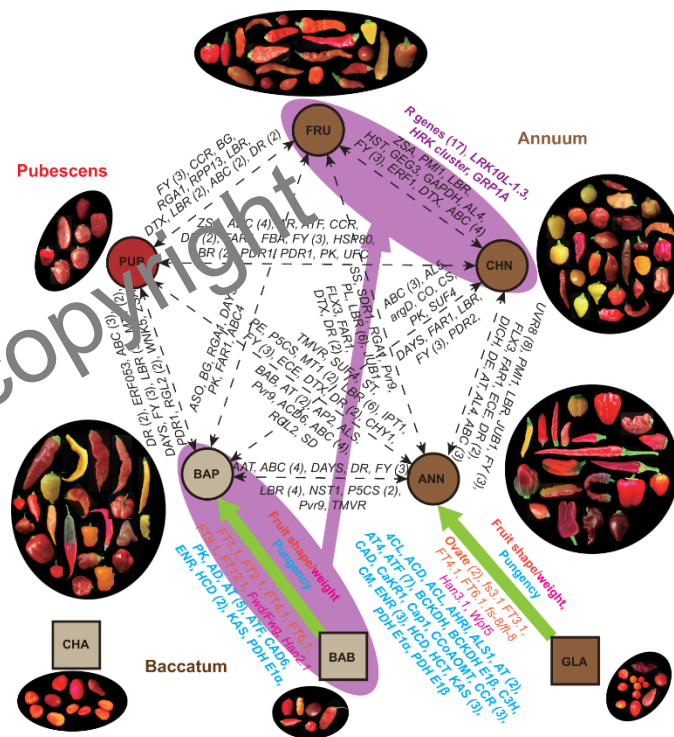
Genomes of cultivated and wild *Capsicum* species provide insights into pepper domestication and population differentiation

Feng Liu, Jiantao Zhao, Honghe Sun, Cheng Xiong, Xuepeng Sun, Xin Wang, Zhongyi Wang, Robert Jarret, Jin Wang, Bingqian Tang, Hao Xu, Bowen Hu, Huan Suo, Bozhi Yang, Lijun Ou, Xuefeng Li, Shudong Zhao, Sha Yang, Zhubing Liu, Fang Yuan, Zhenming Pei, Yanqing Ma, Xiongze Dai, Shan Wu, ... Xuexiao You

☒ + Show authors

[Nature Communications](#) 14, Article number: 5487 (2023) | [Cite this article](#)

28k Accesses | 96 Citations | 103 Altmetric | [Metrics](#)



Lo studio



Obiettivi:

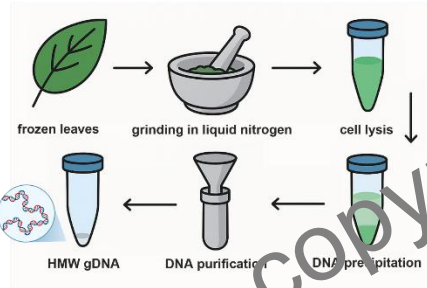
- Assemblaggio dei genomi di varietà di arancio rosso
- Costruzione del pangenoma di arancio rosso

Metodi

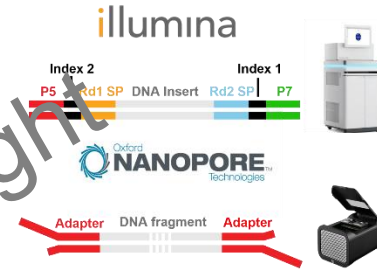
1. Sample collection



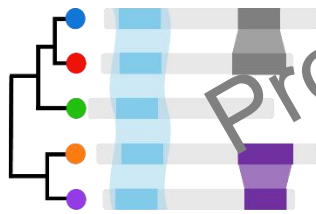
2. gHMW extraction



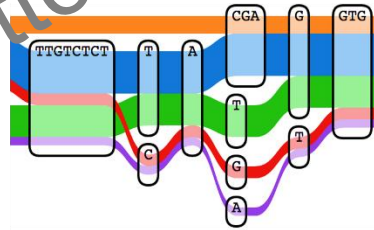
3. Library prep. and Sequencing



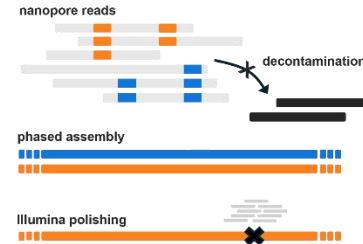
6. Comparative Genomics



5. Pan genome Graph



4. Phased assembly



Proteetto da copyright

Risultati



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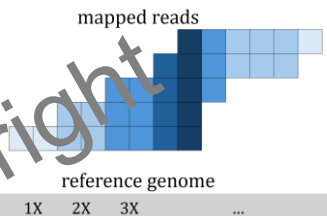


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Sequenziamento



Copertura



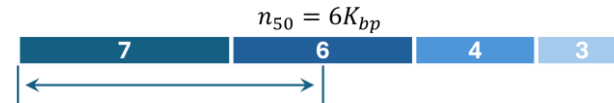
	Output (Gb)	Copertura	ReadQ mediana	N50 (Kb)
<i>Dolce Demmi</i>	20.2	60.2X	25.3	34.1
<i>Inarching</i>	18.2	54.3X	23.0	34.3
<i>Biondo di Tursi</i>	21.4	63.9X	23.4	44.1
<i>Sanguinello Blood Orange</i>	21.6	64.7X	23.3	38.5
<i>Grottammare 7</i>	21.0	62.7X	23.4	29.7
<i>Moro 45</i>	22.3	66.5X	22.6	41.8
<i>Bud Blood</i>	20.5	61.2X	22.8	42.7
<i>Grottammare 11</i>	20.9	62.3X	23.1	41.0
<i>Tarocco Sciarra</i>	22.1	66.0X	22.9	38.4
<i>Sanguinello Ombelicato</i>	22.0	65.8X	23.4	34.7
<i>Washington Sanguinea</i>	22.1	66.0X	22.3	36.6
<i>Tarocchino S Tacle</i>	20.3	60.8X	22.3	33.8

Qualità delle reads

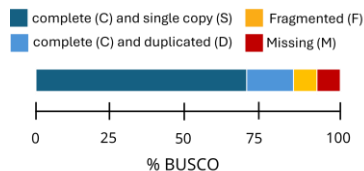
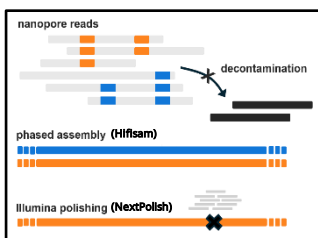
$$\text{baseQ} = -10 \times \log_{10} P$$

P : basecalling error probability

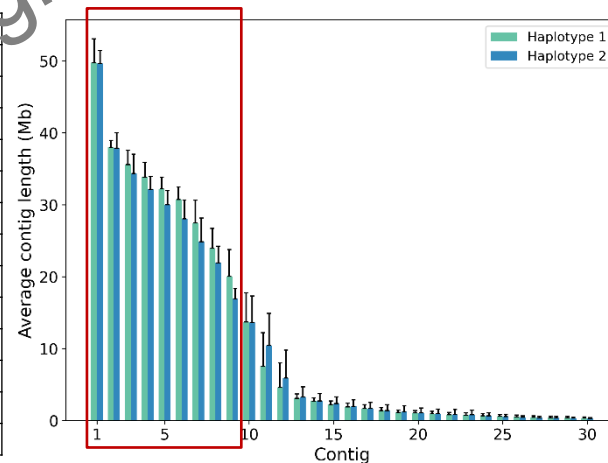
N50



Assemblaggio dei genomi

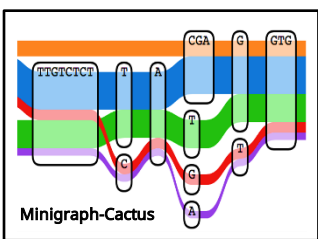


C. sinensis 2n=18

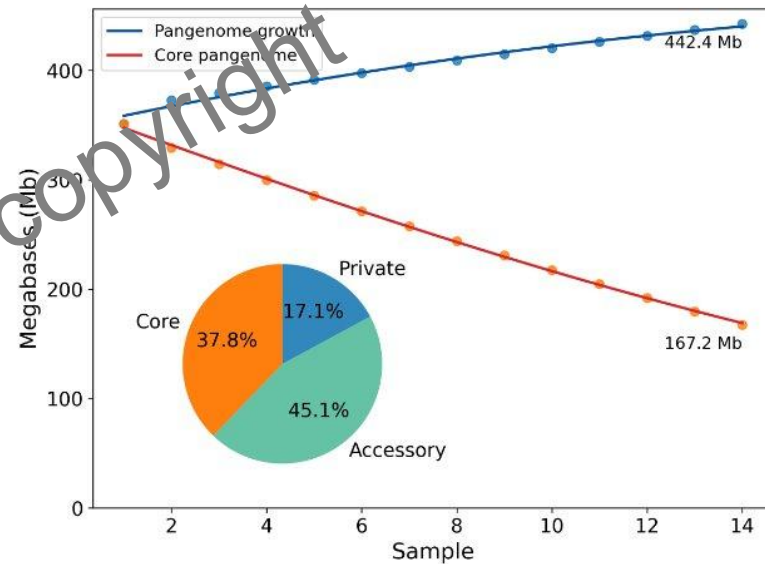
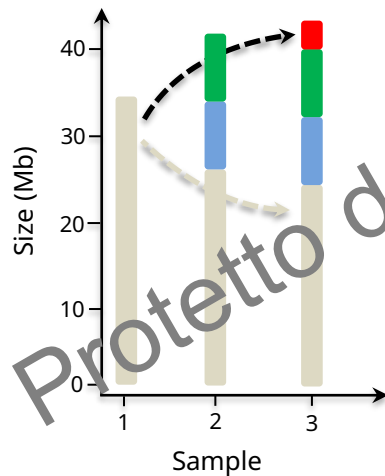
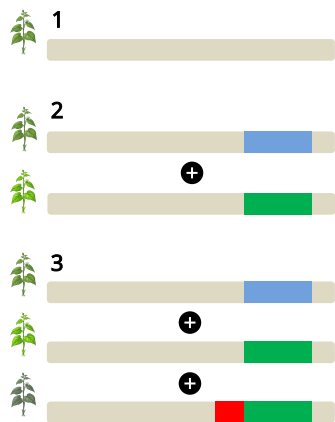


	Dimensione (Mbp)		Contig (N)		N50 (Mbp)		BUSCO* (%)	
	Hap1	Hap2	Hap1	Hap2	Hap1	Hap2	Hap1	Hap2
<i>Biondo di Tursi</i>	337.5	331.9	31	40	33.2	28.1	C:98.0 [S:95.7, D:2.3]	C:97.9 [S:95.7, D:2.2]
<i>Bud Blood</i>	344.2	330.3	50	36	32.9	31.8	C:99.0 [S:97.5, D:1.5]	C:98.6 [S:97.5, D:1.1]
<i>Dolce Demmi</i>	338.0	329.3	42	35	31.7	32.0	C:98.9 [S:97.2, D:1.7]	C:98.0 [S:96.9, D:1.2]
<i>Grottammare 11</i>	340.9	331.6	40	36	36.2	29.5	C:99.0 [S:97.7, D:1.2]	C:98.7 [S:97.2, D:1.5]
<i>Grottammare 7</i>	336.4	334.2	71	53	31.9	30.7	C:99.0 [S:97.5, D:1.5]	C:98.9 [S:97.9, D:1.0]
<i>Inarching</i>	337.6	333.3	75	56	30.8	29.8	C:98.9 [S:97.6, D:1.3]	C:98.9 [S:97.5, D:1.4]
<i>Moro 45</i>	346.3	326.1	36	34	33.3	31.8	C:99.0 [S:97.5, D:1.5]	C:98.0 [S:96.6, D:1.4]
<i>Sanguinello Blood Orange</i>	337.6	329.3	50	40	33.0	31.9	C:98.5 [S:97.3, D:1.2]	C:99.1 [S:97.7, D:1.3]
<i>Sanguinello Ombelicato</i>	331.1	340.8	86	50	29.4	27.2	C:98.8 [S:96.3, D:2.5]	C:99.0 [S:97.8, D:1.2]
<i>Tarocco Sciara</i>	345.2	328.0	53	34	31.9	31.4	C:98.9 [S:97.6, D:1.2]	C:98.9 [S:96.3, D:2.6]
<i>Tarocchino S Tacle</i>	339.6	331.8	84	55	32.0	29.6	C:94.3 [S:90.5, D:3.7]	C:96.4 [S:90.2, D:6.2]
<i>Washington Sanguinea</i>	343.4	327.8	51	68	31.7	26.3	C:99.0 [S:96.9, D:2.1]	C:97.5 [S:96.0, D:1.5]

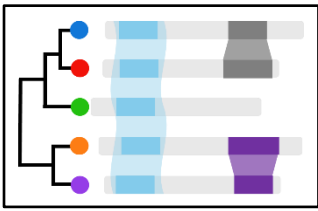
Il pangenoma di arancio rosso



curve di crescita



Prospettive Future



Genomica comparativa:

- Mappatura genetica di caratteri agronomici
- Filogenetica

Ringraziamenti

Prof. Massimo Delledonne

Prof. Marzia Rossato

Prof. Alfonso Esposito



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