



Il Microbioma dei formaggi tipici Siciliani in relazione ai disciplinari di produzione. Esempio di metagenomica applicata



Produzioni casearie tipiche siciliane



Formaggi analizzati e loro caratteristiche

Pasta Filata



Pasta Dura



Prodotti con latte di pecora crudo
in tini di legno

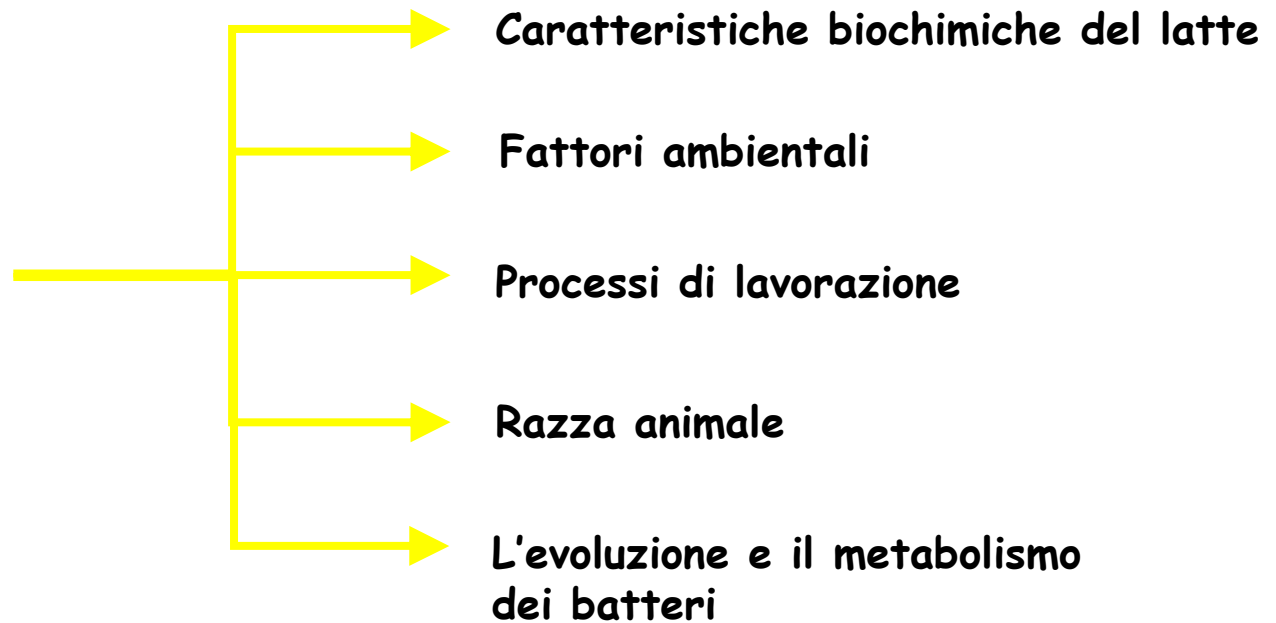
40° C



Formaggi analizzati e loro caratteristiche

Formaggi tradizionali

Ampia varietà
di
caratteristiche
sensoriali



Formaggi e batteri

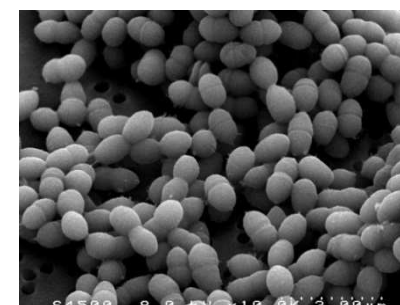
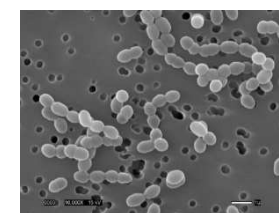
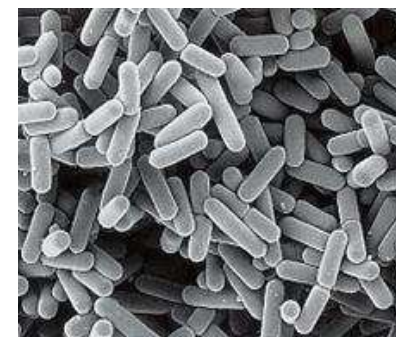
Batterici lattici (LAB)

Lactococcus lactis subsp. *lactis*
Lactococcus lactis subsp. *diacetylactis*
Lactococcus lactis subsp. *cremoris*
Leuconostoc mesenteroides subsp. *cremoris*
Leuconostoc lactis
Lactobacillus acidophilus
Lactobacillus casei subsp. *casei*
Lactobacillus casei subsp. *rhamnosus*
Lactobacillus casei subsp. *pseudoplantarum*

BATTERI
LATTICI
MESOFILI

Streptococcus thermophilus
Lactobacillus delbrueckii subsp. *bulgaricus*
Lactobacillus delbrueckii subsp. *lactis*
Lactobacillus helveticus
Pediococcus acidilactici

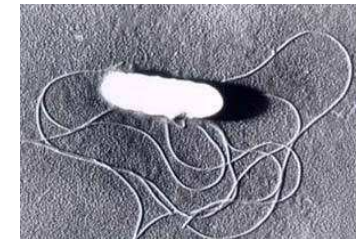
BATTERI
LATTICI
TERMOFILI



Formaggi e batteri

Batterici patogeni potenzialmente presenti

- *Staphylococcus aureus*
- *Listeria monocitogenes*
- *Salmonella spp.*
- *Escherichia coli*
- *Campylobacter spp.*



Importanza dei sistemi di controllo

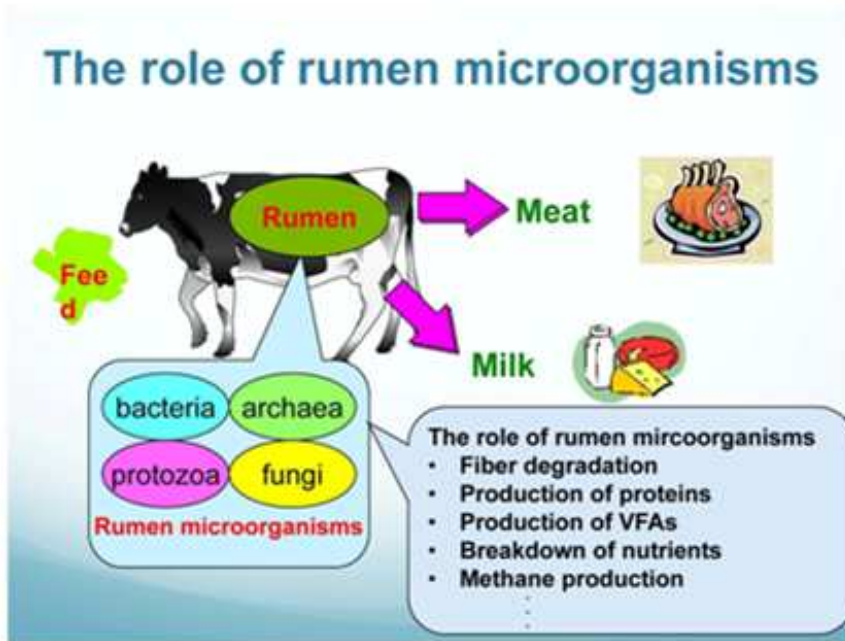
Sicurezza

Qualità

Microbiota Animale



- Lo stato di salute
- Il benessere
- La fisiologia
- pH ruminale
- L'accrescimento
- La composizione del latte (tenore in grasso, in lattosio e proteine)
- la qualità della carne



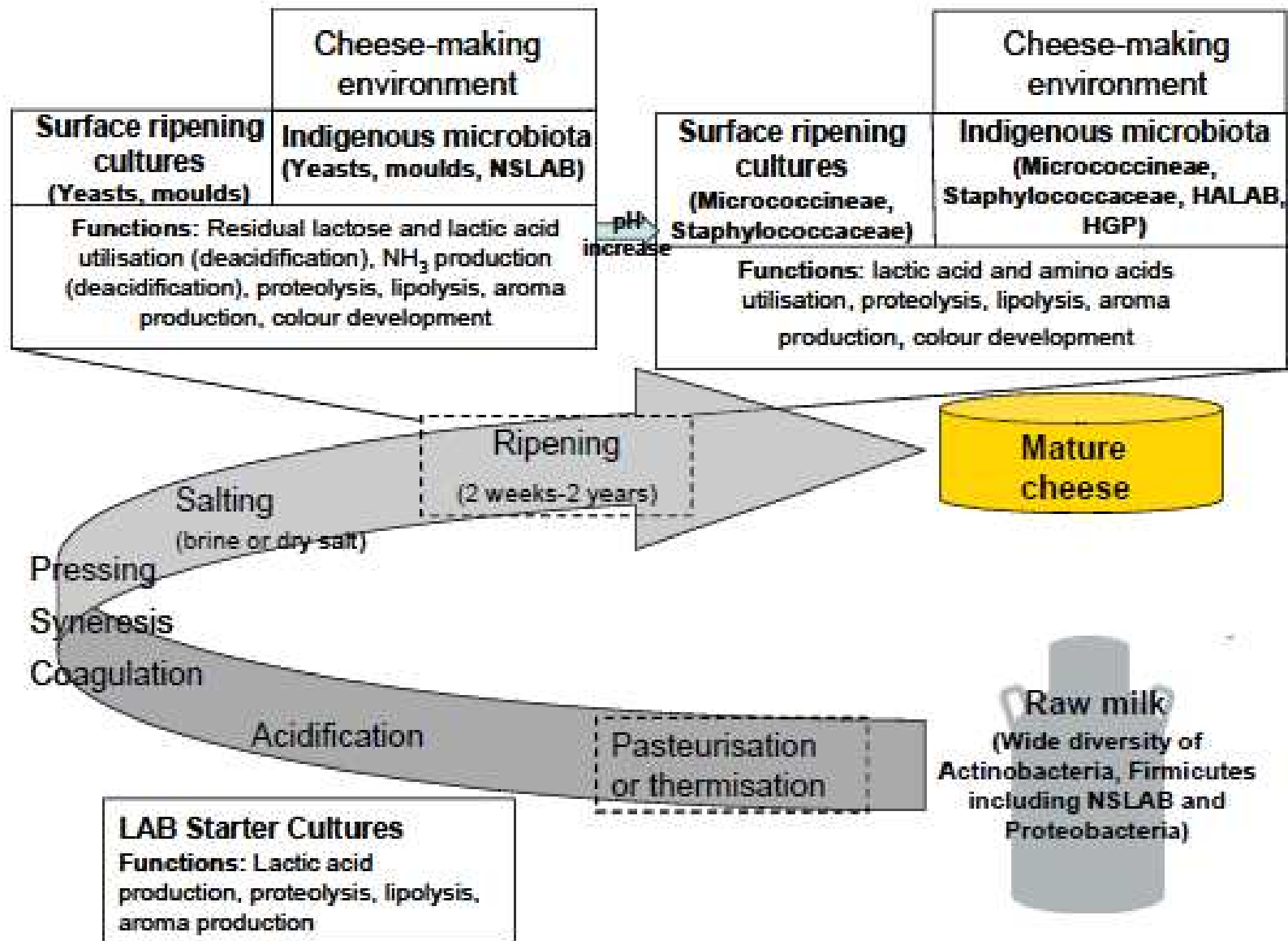


Table 1. Inventory of microbial interactions in cheeses

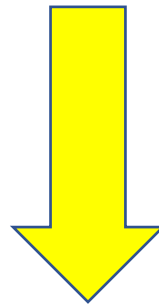
Interaction types	Effect in cheese and / or molecules produced	Microorganisms involved	Microbiological phenomenon observed
Commensalism	Cheese-surface deacidification: Lactic acid utilisation Alcaline metabolites (NH ₃) production	Yeasts, ripening bacteria	Growth of acid-sensitive bacteria
Amensalism	Curd acidification Organic acids (i.e. lactate) Bacteriocins	LAB, spoilage and pathogenic bacteria	Inhibition of acid-sensitive bacteria Lysis of pathogenic and spoilage bacteria
Competition	Harvest of Iron Jameson effect	Siderophores containing bacteria, auxotrophic bacteria Microbiota of wooden shelves, <i>Listeria monocytogenes</i>	Reduced colonization capacity of auxotrophic strains Limited colonization of <i>L. monocytogenes</i>
Parasitism	Failure of fermentation	Phage, bacteria	Inactivation of dominant strains

Abbreviations: LAB, lactic acid bacteria

Scopo del lavoro

Identificazione della composizione batterica (microbioma) dei formaggi attraverso

Vastedda della valle del Belice
denominazione d'origine protetta

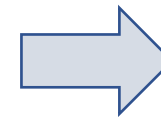


Next Generation Sequencing
(NGS)

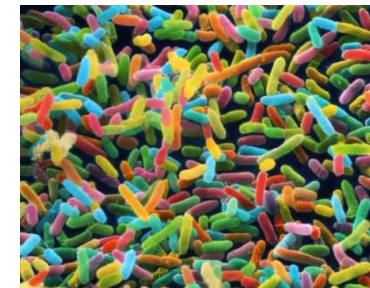
16S rRNA sequencing



**Estrazione
DNA**

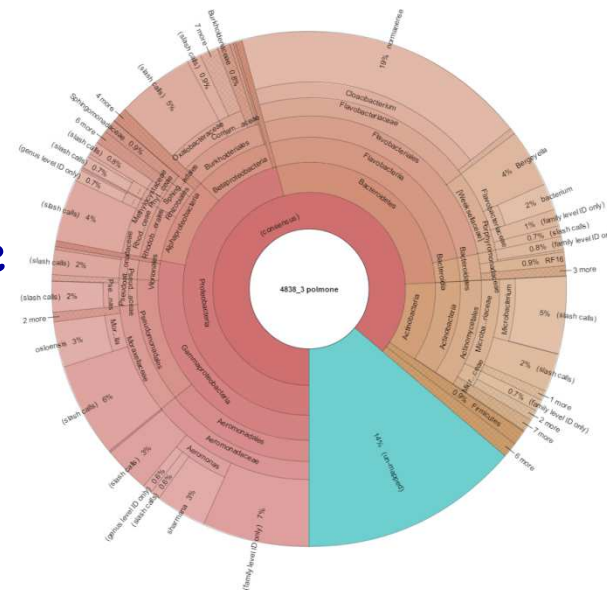


Sequenziamento

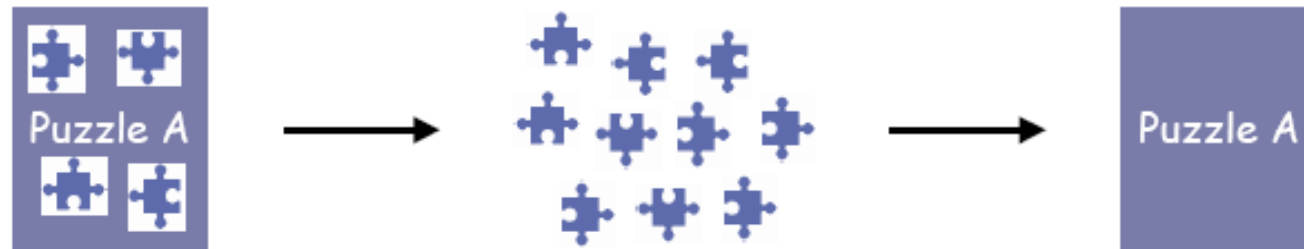


Analisi tassonomica

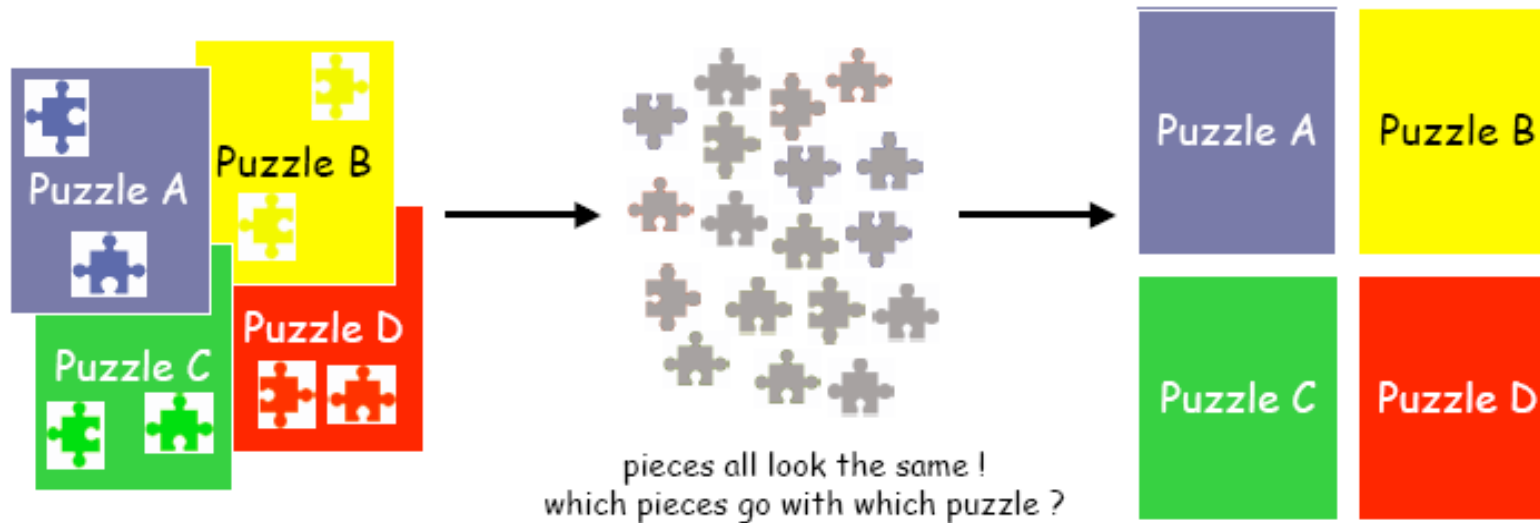
**Caratterizzazione
comunità microbica**
Phylum - classe - ordine
- famiglia - genere -
specie



Isolate genome - single source of DNA



Environmental genome - multiple sources of DNA



Materiali



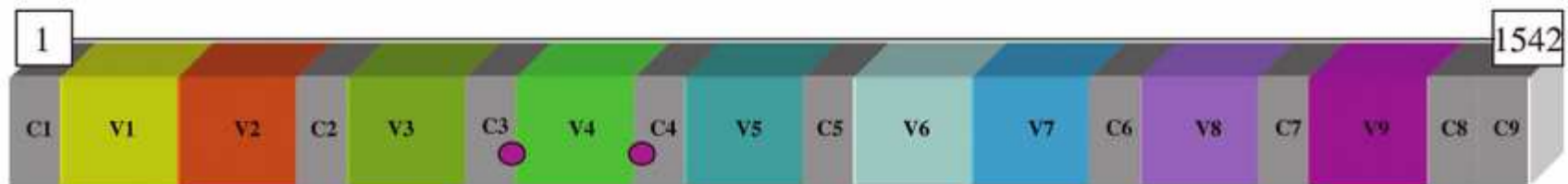
Numero Interno	Proprietà	Specie	Azienda
1	Tino castagno calabrese	Ovina	Izs Sicilia
2	Tino castagno madonita	Ovina	Izs Sicilia
3	Tino Cedro	Ovina	Izs Sicilia
4	Tino ciliegio	Ovina	Izs Sicilia
5	Tino frassino	Ovina	Izs Sicilia
6	Tino noce	Ovina	Izs Sicilia
7	Tino pino	Ovina	Izs Sicilia
8	Tino pioppo	Ovina	Izs Sicilia
9	Tino castagno calabrese	Ovina	Izs Sicilia
10	Tino castagno madonita	Ovina	Izs Sicilia
11	Tino Cedro	Ovina	Izs Sicilia
12	Tino ciliegio	Ovina	Izs Sicilia
13	Tino frassino	Ovina	Izs Sicilia
14	Tino noce	Ovina	Izs Sicilia
15	Tino pino	Ovina	Izs Sicilia
16	Tino pioppo	Ovina	Izs Sicilia
17	Vastedda Listeria	Ovina	Izs Sicilia
18	Pecorino Listeria	Ovina	Izs Sicilia



Metodi

1. Estrazione del DNA

2. Amplificazione del 16S rDNA



NGS

Costruzione di una libreria genomica

Frammentazione del DNA genomico

1

Amplificazione dei frammenti di DNA

2

Purificazione del DNA amplificato

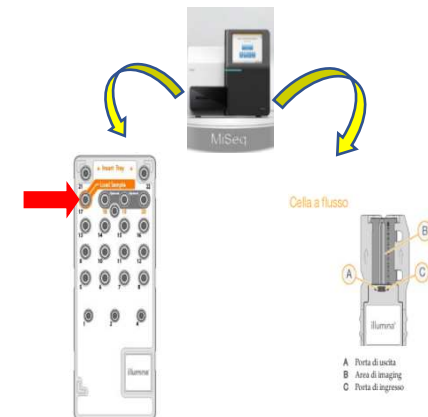
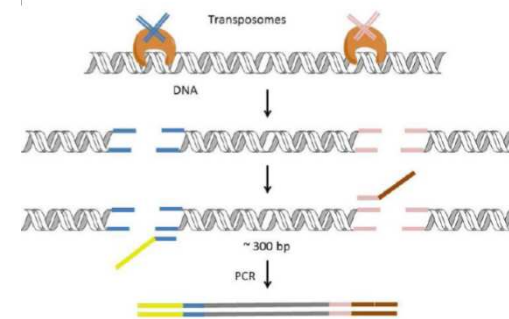
3

Normalizzazione delle librerie

4

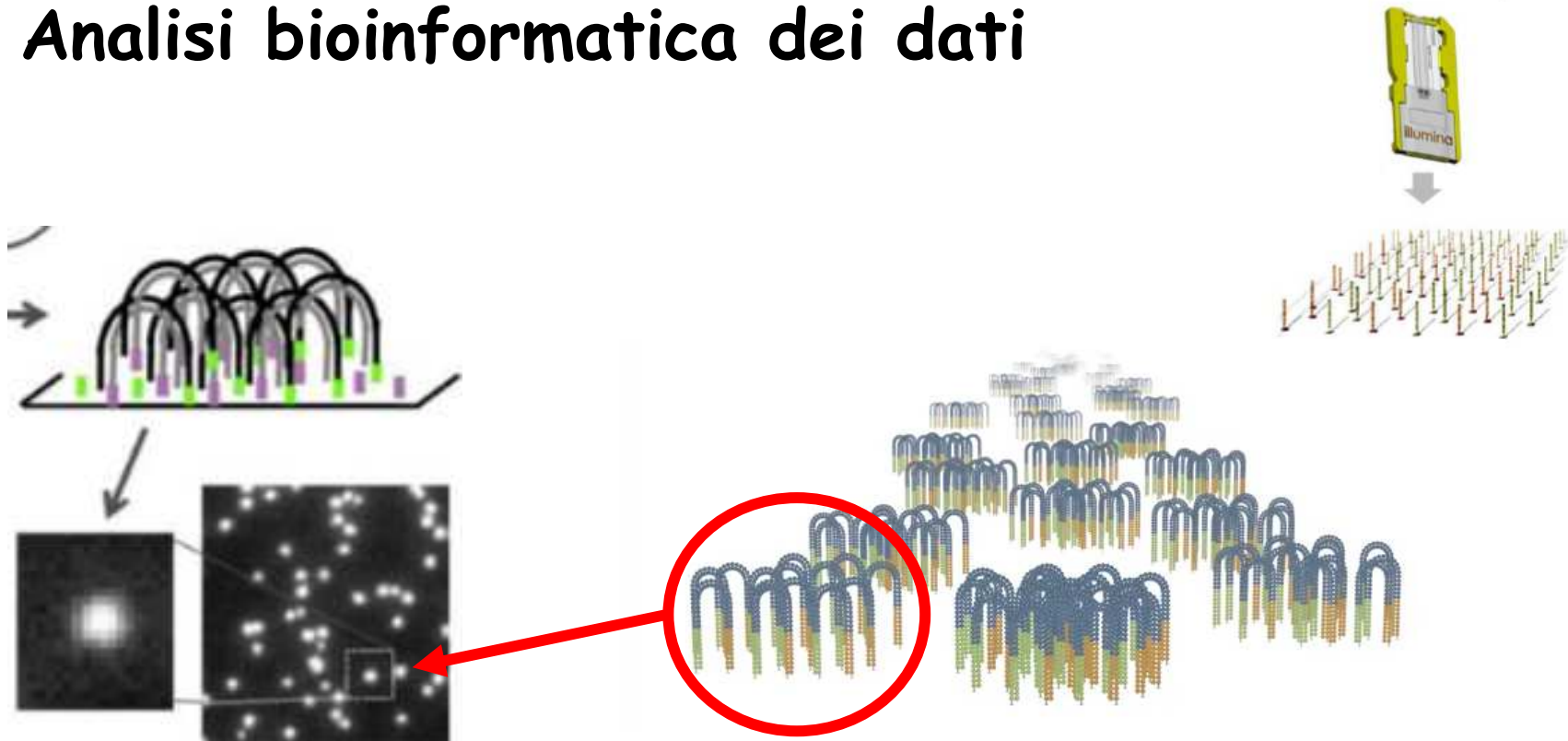
Pool delle librerie

5



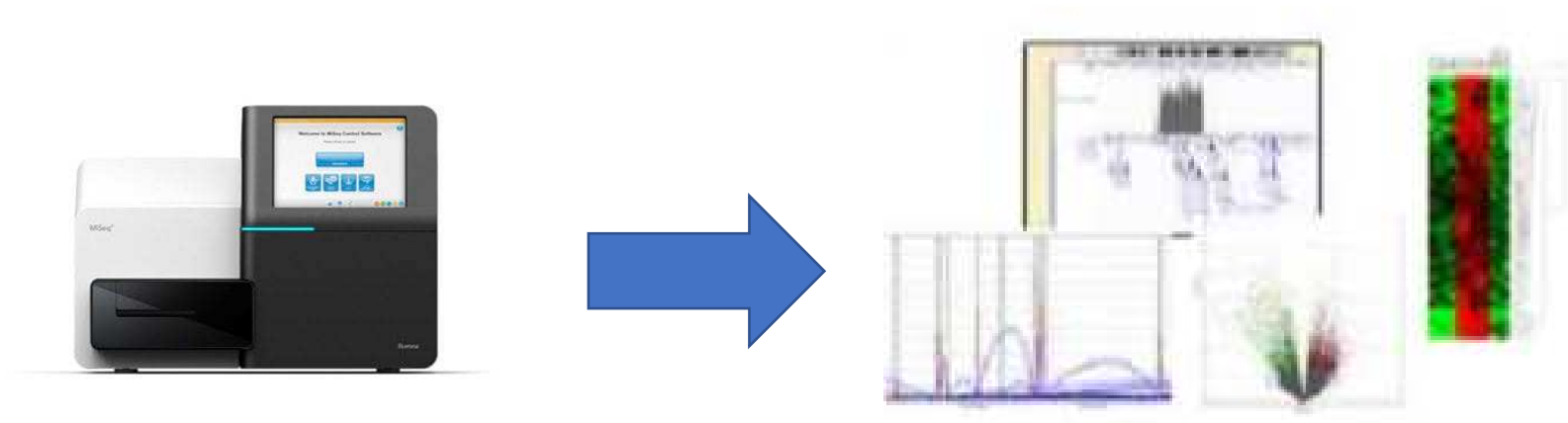
NGS

1. Amplificazione clonale della libreria
2. Sequenziamento ciclico e imaging
3. Analisi bioinformatica dei dati

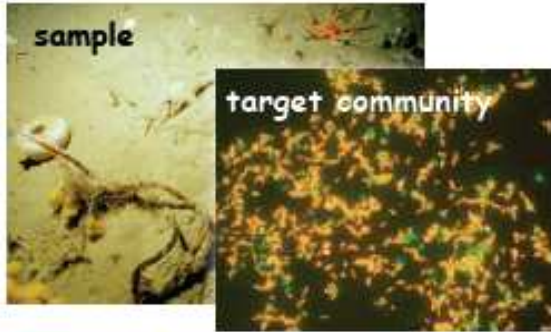


NGS

1. Amplificazione clonale della libreria
2. Sequenziamento ciclico e imaging
- 3. Analisi bioinformatica dei dati**

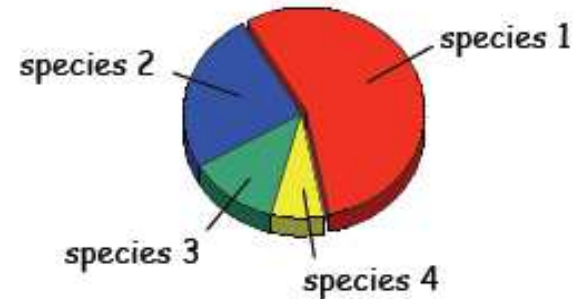
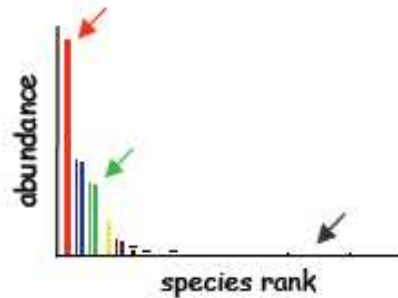


Software MiSeq Reporter (MSR)



Estimation of species richness and evenness

- ◆ 16S rRNA gene library analysis
- ◆ fluorescent in situ hybridization



Genome coverage is proportional to **abundance** in the library

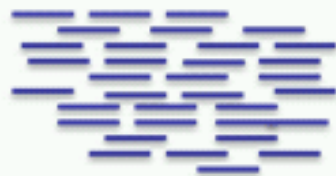


abundant types >> moderately abundant types > rare types

Table 2. Recent applications of bacteriocinogenic cultures and bacteriocins against *L. monocytogenes* in fresh or soft cheeses.

Bacteriocin	Source organism	Mode of utilisation	References
Enterocin 416K1	<i>Enterococcus casseliflavus</i>	Bacteriocin entrapped in polymeric film	[46]
Cerein 8A	<i>Bacillus cereus</i>	Surface application of the bacteriocin	[47]
Enterocin A and B	<i>Enterococcus faecium</i>	Adjunct culture in brine and smearing solution	[48]
Lacticin 3147	<i>Lactococcus lactis</i>	Smearred on the cheese surface	[26]
Nisin and Pediocin PA-1	Recombinant <i>Lactococcus lactis</i>	Starter culture	[49]
Enterocin A	Recombinant <i>Lactococcus lactis</i>	Starter culture	[50]

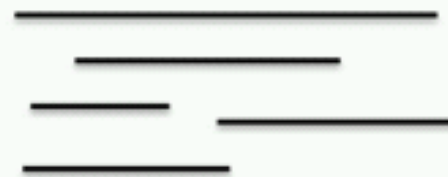
short Illumina
PE reads



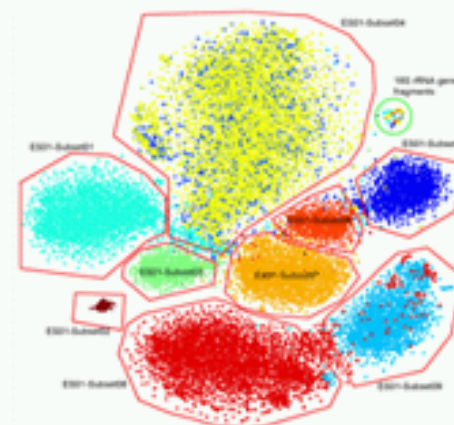
Q-check



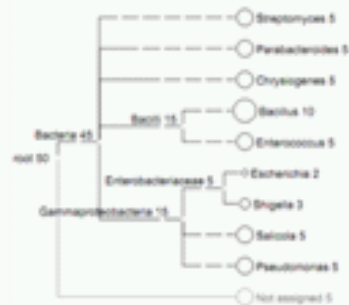
Metagenome
assembly



Genome/contig
binning



Taxonomic
classification

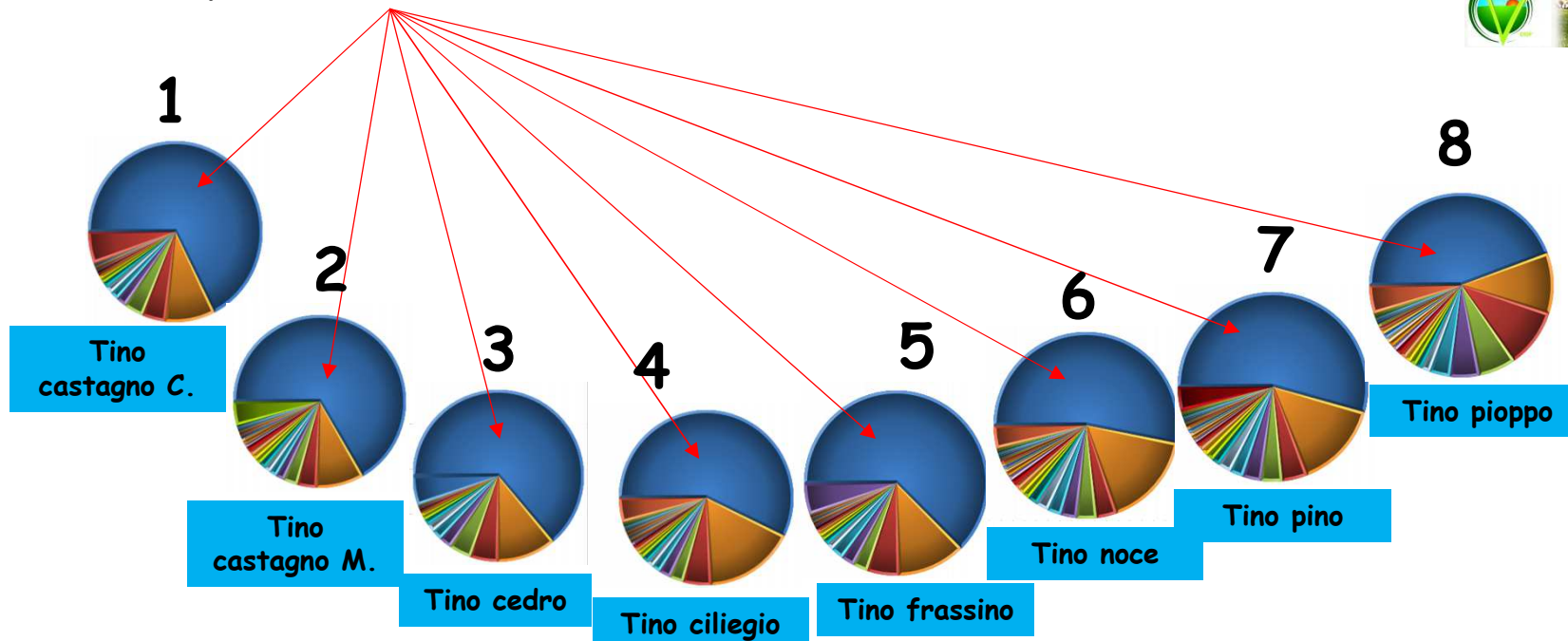


Risultati

Vastedda della valle del Belice
denominazione d'origine protetta



Specie batteriche

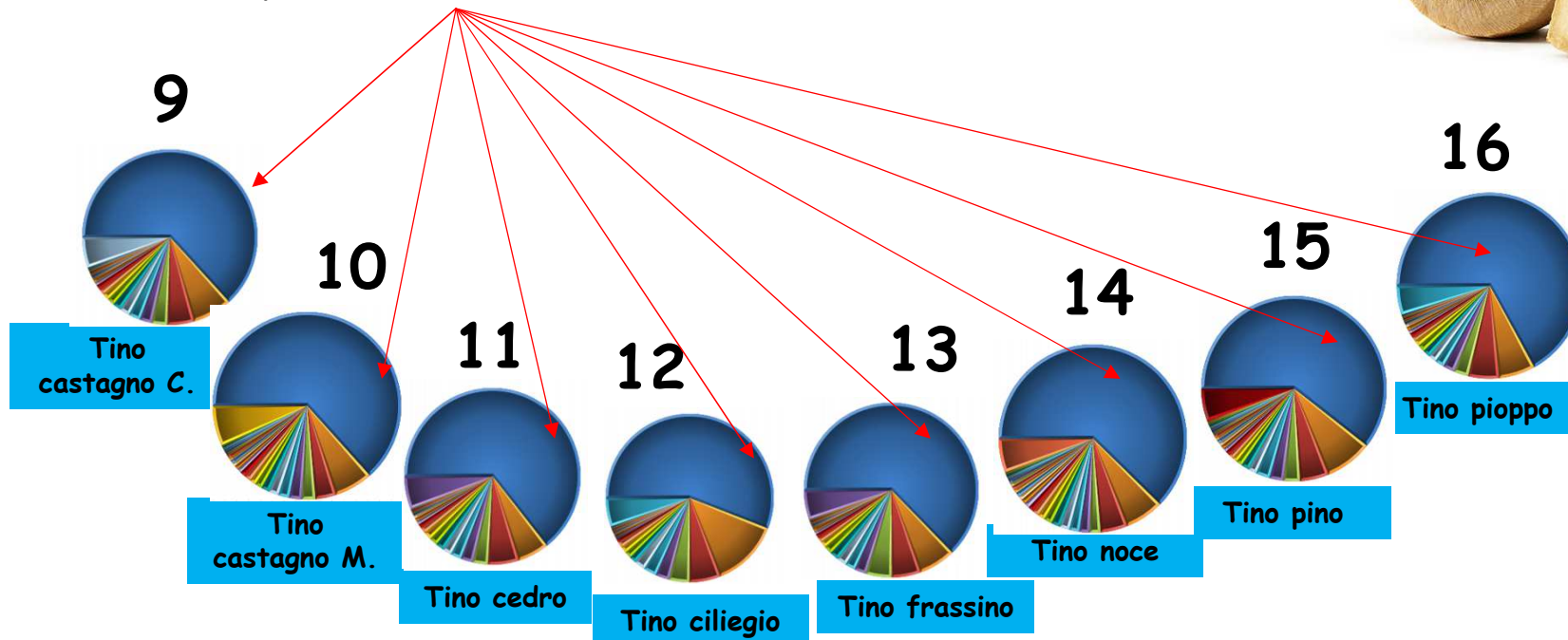


- *Streptococcus pluranimalium* (8-17%)
- *Lactobacillus maniotivorans* (3-10%)
- *Lactobacillus brantae* (2-6%)
- *Streptococcus bovis*, *Lactococcus lactis*, *Lactobacillus parakefiri* (2-5%)
- *Streptococcus equinus*, *Lactococcus fujiensis*, *Enterobacter hormaechei*, *Streptococcus thermophilus* (1-2%)
- Specie batteriche non classificate (40-70%)

Risultati

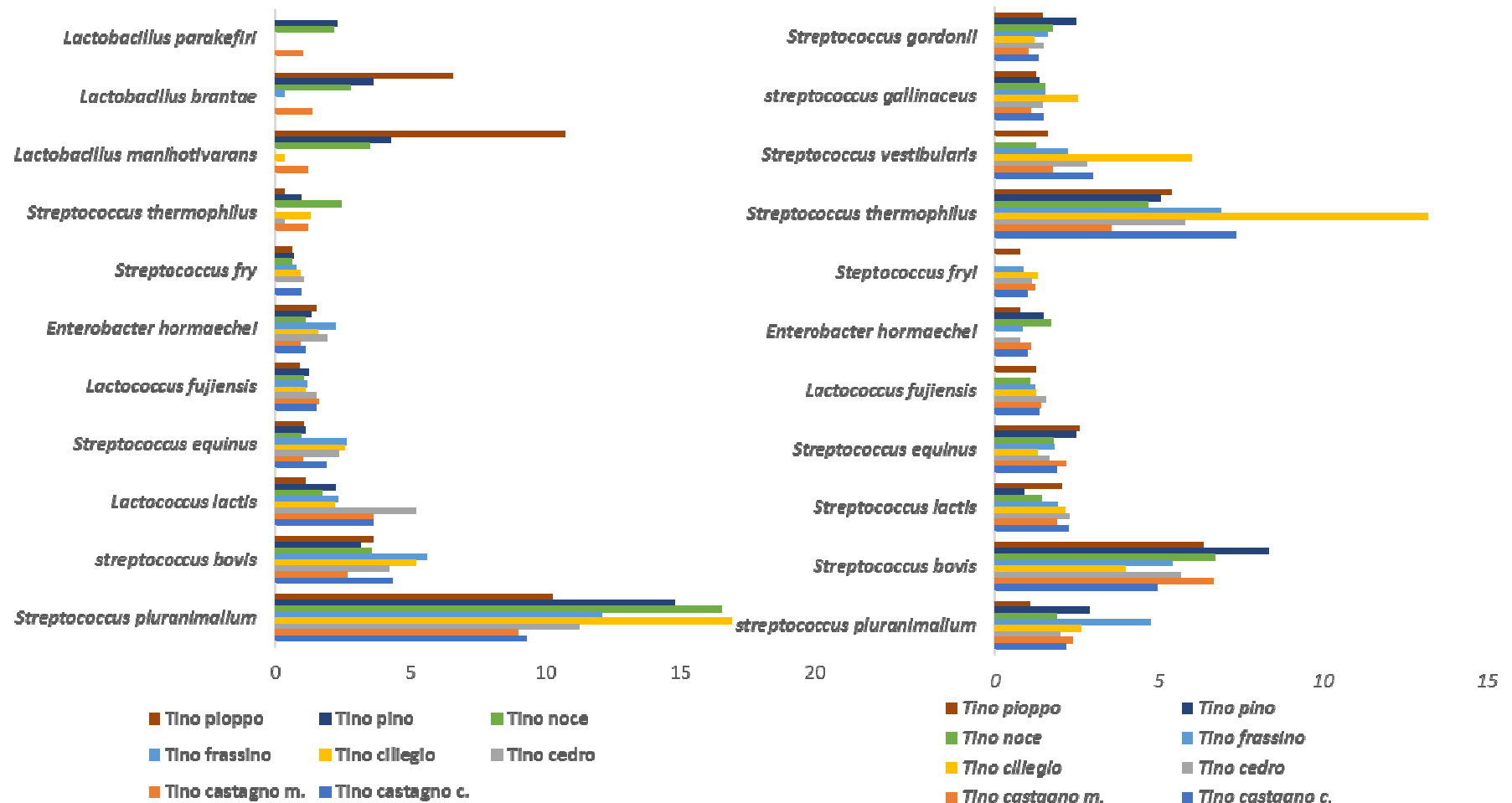


Specie batteriche



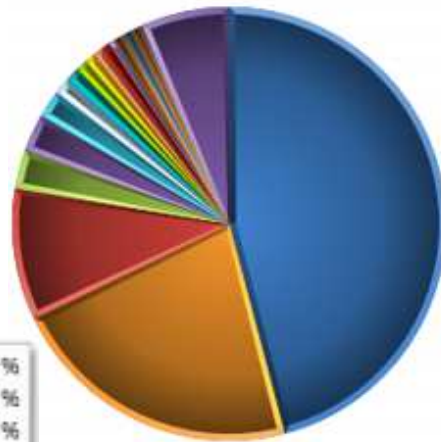
- *Streptococcus thermophilus* (4-13%)
- *Streptococcus bovis* (4-8%)
- *Streptococcus vestibularis* (2-6%)
- *Streptococcus pluranimalium* (1-4%)
- *Streptococcus equinus*, *Streptococcus gallinaceus*, *S. gordonii*, *S. fryi* (1-2%)
- *Lactococcus lactis*, *Lactococcus fujiensis* (1-2%)
- Specie batteriche non classificate (40-70%)

Risultati

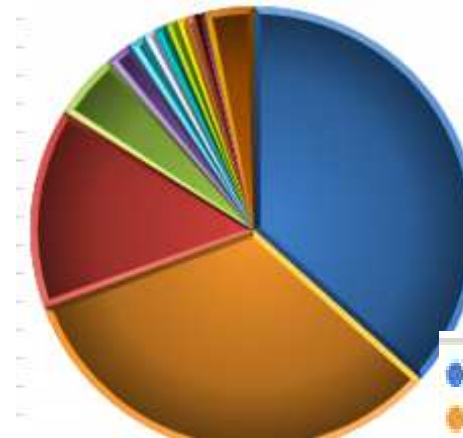


Risultati

Vastedda della valle del Belice
denominazione d'origine protetta



Unclassified	45.87%
Streptococcus pluranimalium	21.92%
Streptococcus thermophilus	9.85%
Streptococcus vestibularis	2.9%
Streptococcus bovis	2.8%
Streptococcus gallinaeus	2.05%
Streptococcus gordonii	1.23%
Lactococcus lactis	1.06%
Streptococcus equinus	0.85%
Streptococcus fryi	0.8%
Lactobacillus rhamnosus	0.75%
Lactococcus fujiensis	0.6%
Lactobacillus parakefiri	0.52%
Acinetobacter johnsonii	0.44%
Lactobacillus parabuchneri	0.43%
Lactobacillus camelliae	0.42%
Streptococcus thoralensis	0.32%
Acinetobacter tjembergiae	0.31%
Streptococcus dentirosetti	0.29%
Other Species	6.59%
Total	100%

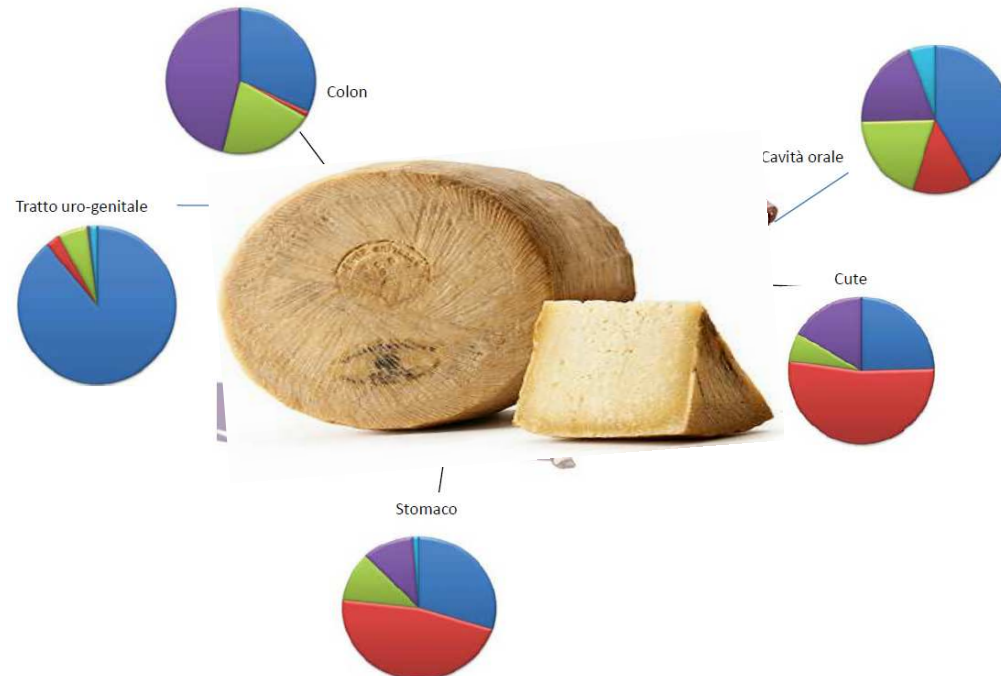


Streptococcus thermophilus	38.62%
Unclassified	32.71%
Streptococcus pluranimalium	14.50%
Streptococcus gallinaeus	4.84%
Streptococcus vestibularis	1.89%
Lactobacillus delbrueckii	1.17%
Streptococcus fryi	0.89%
Streptococcus bovis	0.87%
Lactobacillus rhamnosus	0.82%
Lactobacillus uliginensis	0.78%
Lactobacillus parakefiri	0.53%
Lactobacillus camelliae	0.42%
Streptococcus milleri	0.31%
Other Species	3.59%
Total	100%

Complessità del microbiota

- Le comunità batteriche del FORMAGGI appaiono costituite da un “**core microbiota**”

↓
Essenziale per i
processi di
maturazione



L'alimentazione animale, influenza l'**abbondanza** e la **tipologia** delle OTUs che costituiscono il microbiota del latte e quindi dei formaggi in relazione alla tipologia di lavorazione

Conclusioni

- ✓ Lo studio delle comunità microbiche dei formaggi ha dimostrato che vi è un'abbondante popolazione di batteri la cui presenza è da correlare prevalentemente alle materie prime.
- ✓ L'applicazione delle tecniche di sequenziamento NGS svela la composizione della microflora dei formaggi.
- ✓ La tecnologia NGS potrebbe quindi diventare in futuro uno strumento nella gestione delle filiere produttive nell'industria alimentare per migliorare la qualità e la sicurezza delle produzioni tipiche.



Grazie

