INDUSTRIAL
DIVISION

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READING NATURE

LET'S COME BACK TO
THE ROOTS

Roots causes of microbiological contaminations

CURRENT STATUS OF BACTERIAL IDENTIFICATION

Currently the bacterial isolate identification is done using 16S rRNA gene sequencing. This approach has an important disadvantage, low discrimination power:

The cumulative results from a high number of studies to date suggest that 16S rRNA gene sequencing provides genus identification in most cases (>90%) but less so with regard to species (65 to 83%), with from 1 to 14% of the isolates remaining unidentified after testing [1-4].

Selected Examples Of Bacterial Genera And Species With Identification Problems using 16s rrna gene sequencing.

GENUS	SPECIES
Aeromonas	A. veronii
Bacillus	B. anthracis, B. cere.us, B. globisporus, B. psychrophilus
Bordetella	B. bronchiseptica, B parapertussis, B. pertussis
Burkholderia	B. cocovenenans, B. gladioli, B. pseudomallei, B. thailandensis
Campylobacter	Non-jejuni-coli group
Edwardsiella	E. tarda, E. hoshinae, E. ictaluri
Enterobacter	E. cloacae
Neisseria	N. cinerea, N. meningitidis
Pseudomonas	P. fluorescencs, P. jessenii
Streptociccus	S. mitis, S. oralis, S. pneumoniae

1.- Drancourt M et al. J Clin Microbiol. 2000 Oct; 38(10):3623-30.
2.- Mignard S et al. J Microbiol Methods. 2006 Dec; 67(3):574-81.
3.- Woo PC et al. J Clin Microbiol. 2003 May; 41(5):1996-2001.
4.- Janda M et al. J Clin Microbiol. 2007 Sep; 45(9): 2761–2764.

Although 16S rRNA gene sequencing is highly useful in regards to bacterial classification, it has low phylogenetic power at the species level and poor discriminatory power for some genera and DNA relatedness studies are necessary to provide absolute resolution to these taxonomic problems. The genus Bacillus is a good example of this. The type strains of B. globisporus and B. psychrophilus share >99.5% sequence similarity with regard to their 16S rRNA genes, and yet at the DNA level exhibit only 23 to 50% relatedness in reciprocal hybridization reactions.

TAAG GENETICS BACTERIAL IDENTIFICATION

In TAAG, in order to get higher discriminator power we sequence two genes, the 16S rRNA gene and a housekeeping gene with high phylogenetic power at the species level. Using both sequences, we provide species level results.

BACTERIAL STRAIN TYPING FOR CONTAMINATION SOURCE TRACKING

360º BIOTRACKING PROGRAM

This exclusive state-of-the-art program allows to identify the microorganisms causing any contamination. This is essential for tracking the contaminating microbial source therefore applying the most efficient corrective and preventing actions.

1. Through DNA sequencing, we differentiate the individual pathogens found in the environment.
2. All these individual pathogens are saved in a database.
3. When a pathogen is found in food, we compare its DNA with the pathogen database to identify the exact source of contamination.
4. Once it is identified the contamination source, an effective corrective action can be taken.

SOME OF OUR SERVICES BASE ON DNA SEQUENCING

*TAT: Turnaround time.

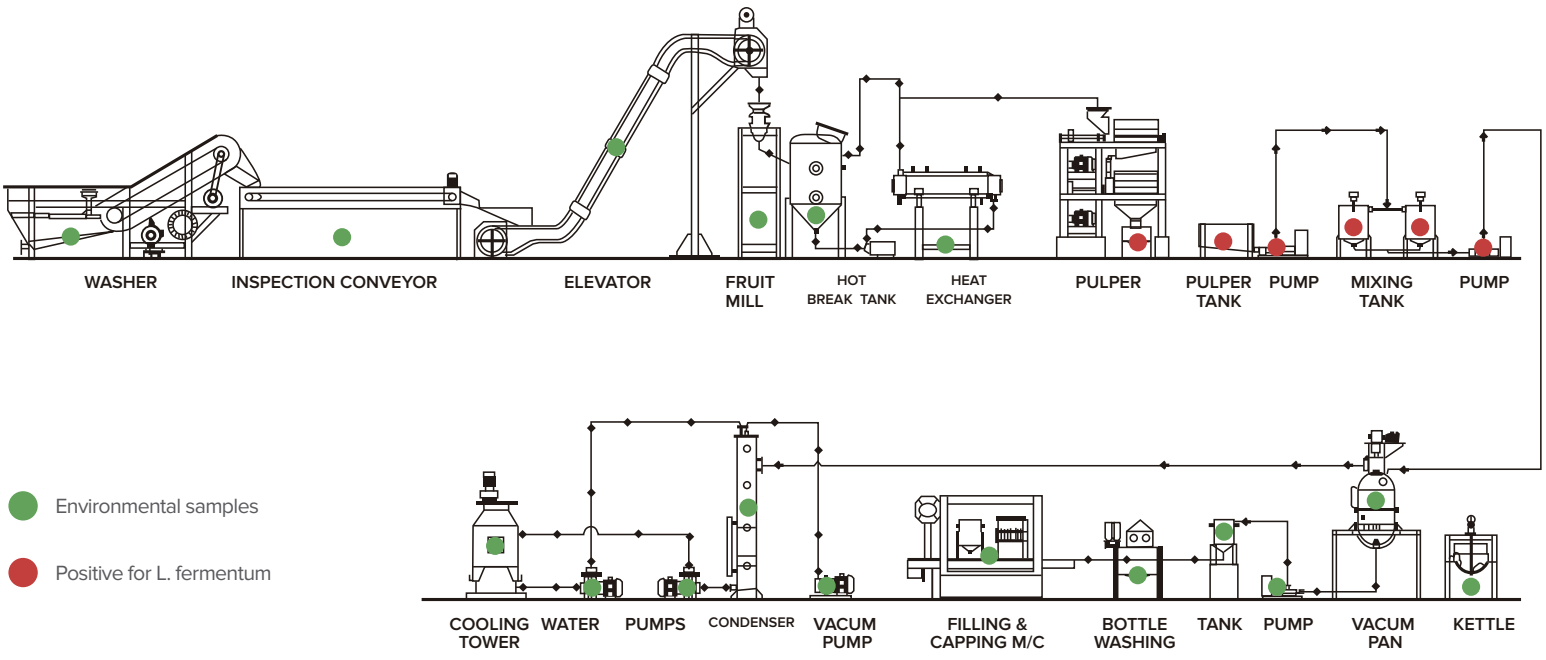
	Traditional Lab			TAAG		
Service	Method	Accuracy	TAT*	Method	Accuracy	TAT*
Bacterial identification from isolate	16S rRNA sequencing	medium	10	16S rRNA and housekeeping gene sequencing	high	5
Fungal identification from isolate	ITS sequencing	medium	10	ITS and housekeeping gene sequencing	high	5
Bacterial identification directly from food products	-	-	-	DNA sequencing directly from food sample	high	5
Bacterial strain typing for contamination source tracking	-	-	-	Sequencing of multiple highly variable genes	high	10

BACTERIAL STRAIN TYPING FOR CONTAMINATION SOURCE TRACKING

Case Study:

An important beverage company had its fruit juices contaminated with Lactobacillus but they could not identify the contamination source. To identify the contamination source, TAAG Genetics did a complete environmental sampling in the plant and additionally we identified the Lactobacillus as L. fermentum. Some environmental samples were positive for Lactobacillus but a few were positive for L. fermentum, indicating that the starting point of the contamination was a cold water pipe used during UHT process. After changing the contaminated water pipe the problem was solved.

Because of this customer requirement, we developed a screening PCR service for detecting Lactobacillus spp and L. fermentum in 72 hrs.



Let's work for safer and quality products

Chile

Río refugio 9641
Pudahuel, Santiago
+56 2 2935 3299
info@tag-genetics.com

China

102#, 1009 Yishan Road Xuhui
Districtl, Shangai
+86 021 64956276
info@tag-genetics.cn

México

Av. Coyoacán #1622
Local 207, Colonia del Valle
Delegación Benito Juarez D.F.
+52 55 52003250
info@tag-genetics.com.mx

www.taag-genetics.com