

DOES FABRIC TYPE DETERMINE IT'S MICROBIAL LOAD? ASSESSMENT FOR RECOMMENDATION IN HEALTH SECTOR

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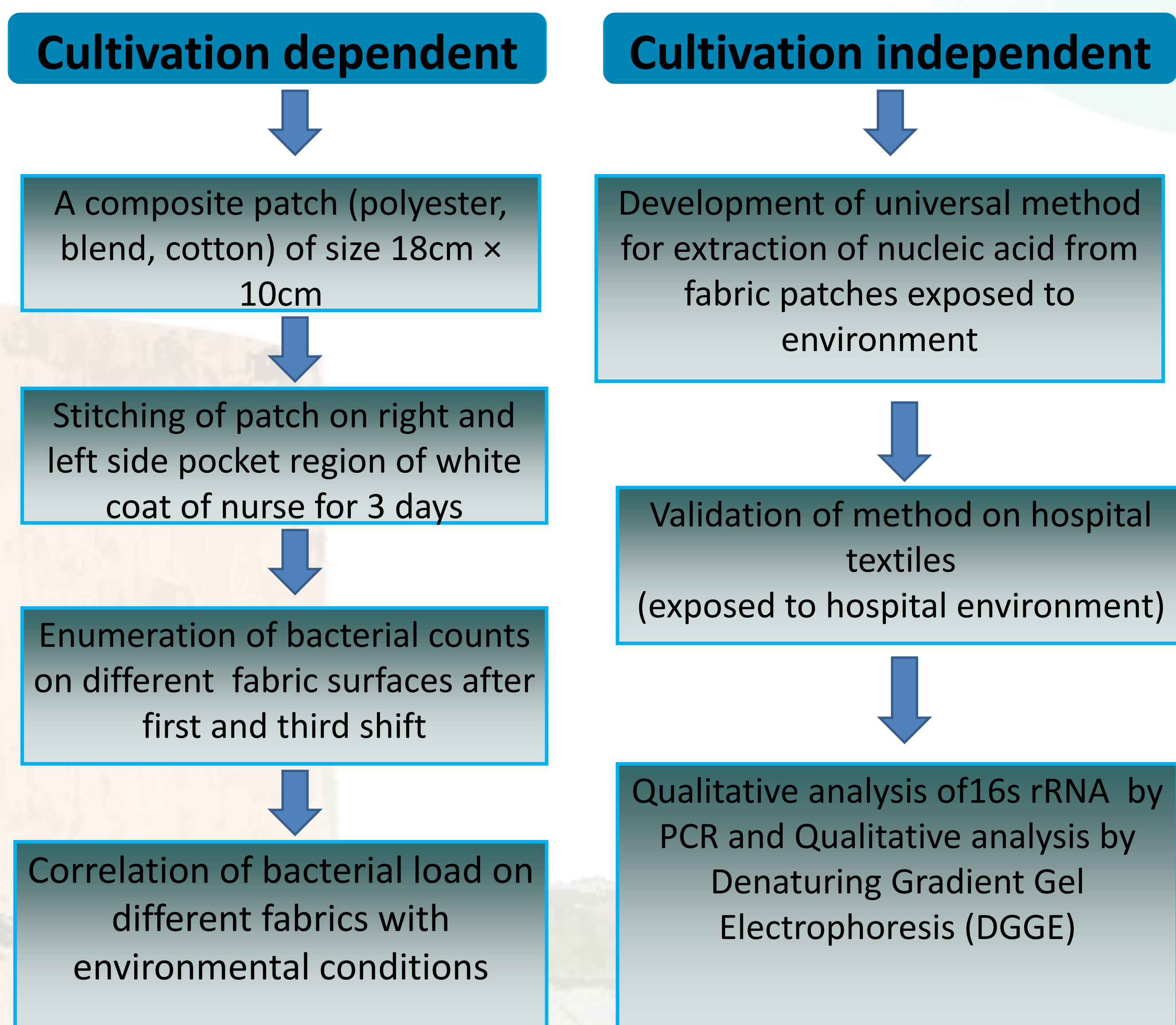
Abstract

Microbe interaction with textile surfaces play an important role in the transfer of nosocomial infection. Uniform of healthcare practitioners act as a vector in the transmission of nosocomial infection. bacterial load (abundance and diversity) was assessed on different types of fabrics *in vivo* to study spatio-temporal dynamics employing culture-dependent and culture-independent approaches.

Introduction

- In healthcare sectors, microbes interact with different textiles (lab coats, bed sheets, curtains etc).
- Microbe-textile interaction plays a significant role in the transmission of nosocomial infections which pose a great threat to human life.
- Uniforms of healthcare workers act as a potential vectors for transmitting the same through endogenous, indirect-contact, besides aerosol transfer of these pathogens in the hospital environment.

Materials and Methods



Conclusions

- Bacterial abundance on nurses' coat is related to the type of fabric used, duration of use and ambient conditions. (Varshney et. al., 2019^a)
- Dynamics of bacterial community could be studied employing the nucleic acid extraction methodology followed by profiling. (Varshney et. al., 2019^b)
- Newly developed method (cultivation-independent) was found suitable for nucleic acid extraction from a variety of fabrics in real life scenario. (Varshney et. al., 2019^c)

Industrial Significance

The propensity of a fabric to attract microbial flora or the "**microbial load**" can be used as a criteria for selection of fabrics for the health and hospital sector.

Result

Bacterial load on different fabrics

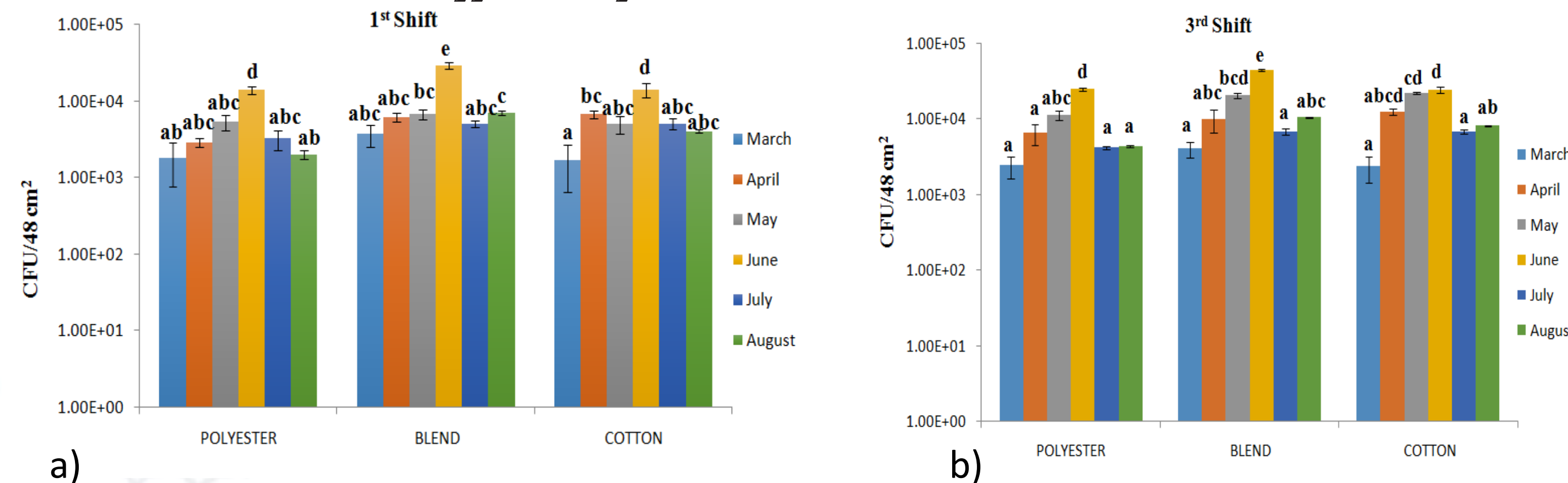


Figure 1: Mean count of bacterial cells detected on test fabrics (March-August) after 1st(a) and 3rd (b) shift. Error bars represent standard deviation (n=3). For all variables with the same letter (a, b, c), the difference between the means is not statistically significant. If two variables have different letters, they are significantly different.

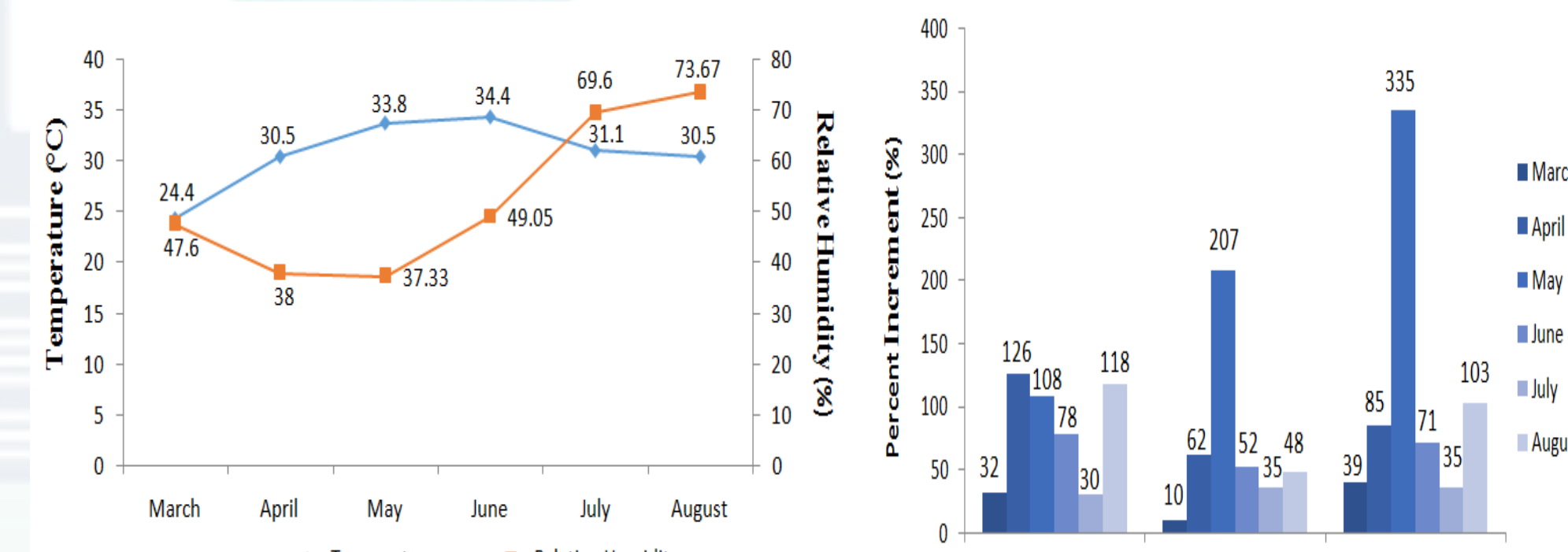


Figure 2: Profile of temperature (°C) and relative humidity (%) in Delhi during March-August 2018

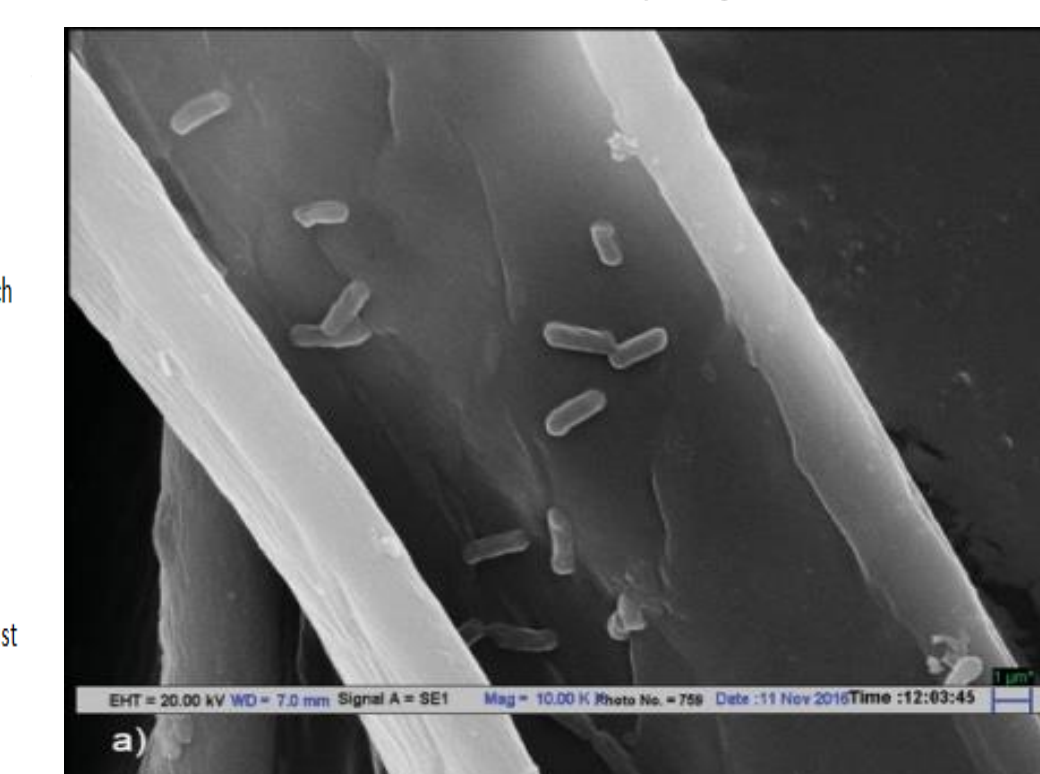


Figure 4: Bacterial adhesion on cotton fibres as viewed under Scanning Electron Microscope

Bacterial Community Profiling using 16S rRNA gene as marker

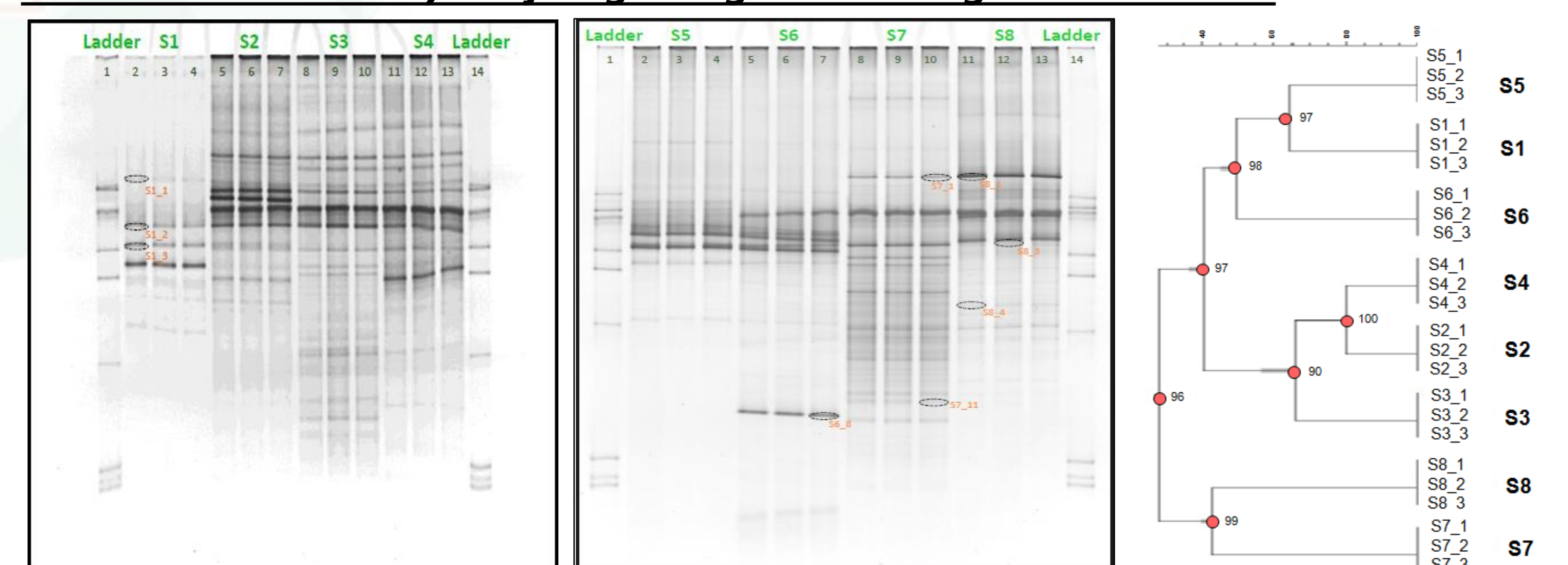


Figure 5: DGGE of fabrics exposed to environment
a) Lanes 1 & 14 - Ladder; Lane 2-4 Sample 1; Lanes 5-7 Sample 2; Lanes 8-10 Sample 3; Lanes 11-13 Sample 4
b) Lanes 1 & 14 - Ladder; Lane 2-4 Sample 5; Lanes 5-7 Sample 6; Lanes 8-10 Sample 7; Lanes 11-13 Sample 8

Figure 6: Dendrogram showing cophenetic correlation among bacterial community profiles generated in figure 5

Sample	Match	Identity (%)	E-value	Accession No.
S8_1	Moraxella osloensis strain CDRc23 16S ribosomal RNA gene, partial sequence	100	0.00E+00	KX503893.1
S8_4	Uncultured bacterium clone JH-YT22 16S ribosomal RNA gene, partial sequence	99	0.00E+00	EF033213.1
S8_3 & S7_1	Uncultured bacterium partial 16S rRNA gene, isolate 1	99	0.00E+00	FM202465.1
S1_2	Pseudomonas sp. Ps14(2012) 16S ribosomal RNA gene, partial sequence	99	0.00E+00	JX411632.1
S1_1	Uncultured bacterium isolate DGGE gel band B17a 16S ribosomal RNA gene, partial sequence	98	0.00E+00	KY062528.1
S1_3	Uncultured bacterium clone JH-YT22 16S ribosomal RNA gene, partial sequence	98	0.00E+00	EF033213.1
S7_11	Pseudomonas sp. Ps8 16S ribosomal RNA gene, partial sequence	97	6.00E-40	AY365082.1
S6_8	Pseudomonas aeruginosa strain AJH3 16S ribosomal RNA gene, partial sequence	97	1.00E-58	KU523263.1

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- S. Varshney***, P. Pandey*, D. Gupta, S. Sharma (2019) Role of fabric properties, moisture, and friction in transfer of bacteria from fabric to fabric. Textile Research Journal, In Press. (* Equal Contribution)

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