ABSTRACT

The increasing usage of dyes across multiple industries, including textiles, tannery, plastics, paper, and paints, has contributed to an alarming increase in both human and environmental exposure to these chemicals. It is well-known that the textile sector in India is a major source of harmful pollutants. The effluent produced by textile factories contains substantial amounts of unfixed dyes, commonly found in wastewater, posing a potential environmental risk. The physicochemical effluent treatment methods are incapable of achieving complete degradation of resistant synthetic dyes in effluents, owing to their lightfastness, stability, colorfastness and decomposition resistance. Biological treatment approaches for dye decolorization have lately gained popularity due to their cost-effectiveness and environmental sustainability, making them applicable to a diverse range of colors. The isolation of microorganisms from contaminated sites is thought to become more successful in treating both refractory and xenobiotic pollutants because they have been acclimatized to the harmful effect of the contaminants. Therefore, it is vitally necessary to have a full knowledge of the biological treatment procedures and many components required to attain the target performance.

In the initial phase of the study, six morphologically distinct bacterial strains were derived from a textile effluent sample obtained from the outlets of textile industrial units and industrial dye-contaminated soil, which exhibited a significant likelihood of contamination by di-azo Reactive Red 120 dyes. A significant number of viable isolates were chosen for further investigation due to their impressive tolerance and optimal decolorization efficiency. The powerful strain was determined to be *Pseudomonas aeruginosa* JU_CHE_01 determined through morphological and biochemical profiling along with 16S rRNA gene analysis. Next, the NCBI Gene Bank database was updated with the 16S rRNA gene sequence. The unadulterated bacterial strain was assessed for the removal of six model azo dyes: Reactive

Red 13, Acid Black 194, Methyl Orange, Reactive Yellow 135, Congo Red, and Direct Violet 1. This strain demonstrated tolerance to elevated dye concentrations, achieving maximal decolorization for all six model colors. Consequently, microorganisms capable of digesting Reactive Red 120 (RR120) dye shown remarkable efficacy and metabolic adaptability.

Five process variables were assessed for optimal conditions utilizing the Taguchi methodology. Two media components (glucose and yeast extract) and three physicochemical parameters (pH, temperature, and inoculum dose) were improved due to their substantial effects on RR120 biodegradation. The L-18 Orthogonal Arrays (OA) framework was employed in the design of many experimental researches. The L-18 Orthogonal Arrays (OA) framework was employed in the design of many experimental researches. To determine the crucial elements and ideal circumstances for increasing RR120 dye breakdown, the obtained experimental findings was examined employing the Signal-to-noise (S/N) ratio and a "bigger is better" methodology. The validation of the expected data by confirmatory investigations demonstrated that under optimal conditions of yeast extract and glucose, each at 1 g/L concentration, 8 pH, 37°C temperature, and 10% (v/v) inoculum dose, a 97.63% degradation of the RR120 dye could be attained within 48 hours, resulting in a 66.75% improvement in RR120 degradation. ANOVA revealed that the carbon (glucose) and nitrogen (yeast extract) sources significantly affected RR120 biodegradation, contributing 27.933% and 19.526%, respectively, followed by pH at 4.664%, temperature at 13.476%, and inoculum dose at 28.951%.

This work clarifies the kinetics of facultative anaerobic biological growth and the degradation of RR120 using the isolated bacterium *Pseudomonas aeruginosa* JU_CHE_01, which can decolorize 600 mg L^{-1} of RR120, marking the highest concentration recorded for biodegradation to date. The results from the batch degradation experiments revealed that

Pseudomonas aeruginosa JU_CHE_01 demonstrated substrate inhibition kinetics, with the Haldane model accurately representing this research outcome. The biokinetic parameters employed for the growth of biomass estimation included a maximum specific growth rate of μ_{max}= 0.18 h^{-1}, a half-saturation coefficient of K_s = 345 mg L^{-1}, and an inhibition coefficient of K_i = 83.34. A post-treatment research was conducted to assess the phytotoxicity of the biodegraded products by germination of seed and root elongation assays on *Cicer arietinum, Vigna mungo,* and *Vigna radiata*. The results indicated a significant reduction in phytotoxicity during biodegradation, along with improved germination rates and assessment of root growth in treated specimens against control groups. The findings demonstrate that the bacterial strain effectively eliminates RR120 and mitigates its harmful environmental impacts. This work demonstrates the effectiveness of bacterial biodegradation in addressing high-concentration textile dyes like RR120, with kinetic modeling providing valuable insights for process enhancement. The decrease in phytotoxicity confirms the environmental safety of the biodegraded products, promoting the advancement of sustainable wastewater treatment techniques.

Keywords: Azo dye, Reactive Red 120 dye, Biodecolorization, Optimization, Kinetics