



Detection Indigenous Microorganism of Dyeing Textile for Waste water treatment

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Abstract : Industrial waste becomes one of the factors causing river pollution. Dye-containing wastes from this industry is one of the most difficult waste water to be repaired because the content of toxic compound. Processing for color removal of textile waste using a yeast that has the ability to decompose the carbon chain. The purpose of study is to know yeasts living in waste. The sample taken directly from the wastewater in the textile company, then analysis using YST identification (ID) card system, the results seen on panel table color change with positive or negative. The results of isolate identification were *Yarrowia (Candida) lipolytica* 99,9%, *Blastoschizomyces capitatus* 99,87%, and *Candida rugosa* 79,17%. Three species have the ability for wastewater treatment.

Key words : Indigenous Microorganism, Dyeing Textile, Wastewater, Treatment.

Introduction

Textiles and textile products is one of the main export products of Indonesia. The population in the world that continues to grow to make the level of consumption or the world market demand for textile products increased. This can be an opportunity for producers and processors of textile products to continue to increase market prices domestic and international. However, due to the development of the industrial company, most of it produces wastewater and dumps it into the Cikijing River. The results of its production process and its wastewater discharge are thought to contribute significantly to the increased pollution load of the river. Rancaekek is one of the industrial development areas causing the decrease of agricultural production, and the decreasing of agricultural area. Cases of environmental pollution and destruction of rice crops in rancaekek rice fields have a negative impact on the development of the textile industry in agricultural production areas (Sayori, 2017).

Under the terms of waste discharged into the environment it should be safe for the biophysical environment of the land, water bodies and human and animal health. The wastes are diverted to the Wastewater Treatment Installation and the processed before they are discharged into the environment. But in reality, the

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waste is often people complain because of the negative impact arising from the disposal of such waste. As a result of industrial waste disposal also causes the surrounding environment or into the river flow causing disruption of the river basin ecosystem, ranging from non-fulfillment of quality water standard colorless, smelly, and non-toxic (Nilanjana & Charumathi, 2012).

According to Astirin & Winarno (2000), the main problem of this waterwaste is the smell, which shows the biodegradation process is less than perfect. Smelly caused by anaerobic decomposition by microorganisms. The anaerobic process occurs because of the lack or absence of oxygen. The next problem is the emergence of color in the waste water, because in the dye fabric not all the dye will be absorbed by the cloth, so it will cause the remnants of dye.

Processing to remove the color of textile waste using yeasts that have the ability to decipher the carbon chain. Textile dyes are mostly organic compounds (both natural and synthetic dyes) comprising a structure that produces a color called chromogen, an aromatic body that contains a color-giving group, commonly called a chromophore. Chromophore are clusters that cause color by selective wavelength absorption (Bajpai *et al.*, 1993).

The appearance of color is supported by the presence of R in this case cyclic carbon compound. If the chain is disconnected then the color will disappear, as well as if there is saturation in double bond or double bond termination. The use of microbes is one of the alternatives to eliminate color by breaking the cyclic chain or double bond (Bergbauer *et al.*, 1991).

This study aims to determine the type of yeast that is able to decompose the textile wastewater.

Materials and Methods

Samples of waste are taken directly from the PT Kahatex textile factory, West Java. Then the samples were analyzed in biochemistry laboratory of Medical Faculty of Padjadjaran University.

The isolation medium used is YMA (yeast & mold agar). Isolate taken from the sample origin, dilution was made up to 10^3 then pour plate method with the addition of YMA media. Incubated for 48 hours 27°C and then selected in macroscopic and microscopic. Then purified, and got some isolate that is sp S1 10^{-1} , sp S1 10^{-2} , sp S3 10^{-1} , sp S3 10^{-2} and sp S3 10^{-3} . Isolate in streak triplo to YMA media for stock isolate.

Method RapID test

Test to detect yeasts based on the concept of lateral flow immunoassay systems. Briefly for the examination taken each yeast isolates using swabs inserted into each test tube and in vortex to equalize the turbidity. Then each test tube is inserted into the yeast plus panels. Open the panel cover above the inoculation port by pulling the tab marked "Peel to Inoculate" up and left.

Using a pipette, gently smooth the entire water inoculation tube into the top right corner of the panel. Close the inoculation panel back panel by pressing the peel-back tab back in place. After adding test suspension, and keep the panel on a flat surface, then tilt the panel at an angle of about 45 degrees. Incubate panels inoculated at 30°C in incubators for 4 hours. Then after 4 hours seen the color change. After that add 1 drop of reagent A to panel tube 7 (NAGA) up to 14 (PCHO). Add 1 drop of Reagent B to tube panel 16 (PRO) up to 18 (LGY).

After the addition of Rapid Yeast Plus Reagent B, leave at least 30 seconds but not more than 1 minute for the color change. Read and test test tube values from left to right using the interpretation guides presented in the score table records in the appropriate boxes on the report form. The micro reference code obtained on the report form is entered in the ERIC for identification.

Result and Discussion

Results of isolates S110⁻², S310⁻¹,

and S310⁻³ show macroscopically, isolate A color of cloudy white colony, subtle fringes of colonies, then isolate B showed cream-white colonies, multi-folded colonic surfaces and uneven rims. Isolate C forms colonies of milky white surface surface convex and smooth colonies.

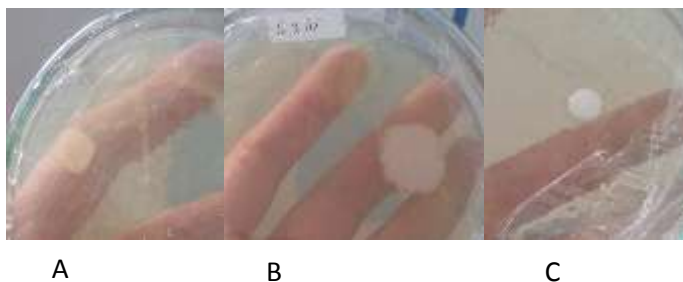


Fig 1. Macroscopic Colonies S110⁻² (a), S310⁻¹ (b), and S310⁻³ (c).

Microscopic isolates can be seen in Figure 2. Issues S110⁻² have an oval cell shape (speroid), forming an elongated ellipse (6.27 μ m), reproduction of the budding process (Figure 2a). Isolate S310⁻¹ cells form a flat cylinder (7.02 μ m), do not perform the budding process (figure 2b). Cells in isolate S310⁻³ are ovoid, cylindrical (6.69 μ m), single, paired, and clustered, multilateral budding reproduction (Figure 2c).

After a microscopic and microscopic observation, a RapID test was conducted to determine the species species of the isolates.

The results of Rapid Test seen from the color change panel substrate so that the positive or negative results, which can be seen in table 1.

Tabel 1. Results of Rapid Test Substrate Panel.

Isolate	Result
S110 ⁻²	LIP (+), β glu (+), PCHO (+), PRO (+) dan HIST (+).
S310 ⁻¹	GLU (+), LIP (+), HIST (+), dan LGY (+).
S310 ⁻³	HIST (+)

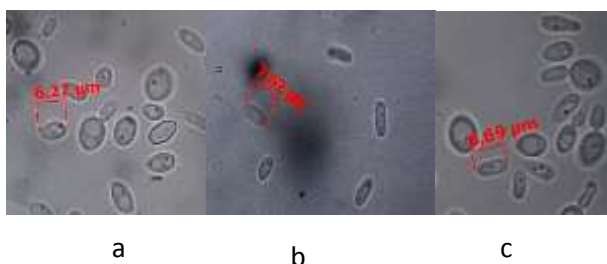


Fig 2. Microscopic Colonies S110⁻² (a), S310⁻¹ (b), and S310⁻³ (c).

Result of isolate S110⁻² concluded that isolate need fatty acid characterized by yellow color change and able to hydrolyze enzymes such as p-Nitrophenyl- β , D-glucoside become yellow cloudy, p-Nitrophenyl phosphorylcholine pink, Proline- β -naphthylamide color pink, and pink histidine β -naphthylamide. Isolate S310⁻¹ results obtained to absorb glucose is characterized by yellow clouding, absorbing fatty acids into light yellow

and hydrolyzing enzymes Histidine β -naphthylamide converts into pink and Leucyl-glycine β -naphthylamide into pink. From S310⁻³ known only able to absorb or lyse Histidine β -naphthylamide characterized by pink change.

After the panel results are known then continued using the software ERIC (Electronic RapId Compendium). The results showed that the result of isolate S110⁻² identified *Yarrowia lipolytica* with 99.9% probability value can be seen in figure 3.

ERIC Web	Identification Report		
RapID Yeast Plus		Run Date: 26/02/18	
Microcode: 144827		Facility: Padjadjaran University Subangsa (U)	
System Tests -GLU 024 -TSE 024 -GAG 024 -GPG 024 -PSE 024 -PRG 024 -HGL 024 -GAP 024 -HGLT 024 -HGL 024 -PGR 024 -HGLT 024 -EGC 024 -LTP 024 -GGLT 024 -GPG 024 -GSE 024 -LTP 024			
IDENTIFICATION = <i>Yar. lipolytica</i>			
Clones	Probability	Strains	Contradictions
<i>Yar. lipolytica</i>	99.9%	1170	GLU [R]
<i>Tr. longii</i>	0.0%	141203	NAGA[7] LNE [7]
Probability Level: Adequate Deficiency: Acceptable			
Test	<i>Yar. lipolytica</i>	<i>Tr. longii</i>	
Mattson	+	+	36
Sucrose	+	+	36
Lactose	+	+	36
Gelatin	+	+	36

Fig 3. Identification of Khamir using Electronic Rapid Compendium.

Yarrowia lipolytica is a microaerophilic yeast. This has complete cell immobilization for the degradation of different compounds in wastewater and has several other advantages such as providing high activity, yield, and good stability and capable of separating cell mass from wastewater to allow for reuse. Occasionally, *Y. lipolytica* was also found with a supposedly hostile environment for growth of *Yarrowia* (Wu Lan et al., 2009; Roostita & Fleet, 1996).

ERIC Web	Identification Report		
RapID Yeast Plus		Run Date: 26/02/18	
Microcode: 144827		Facility: Padjadjaran University Subangsa (U)	
System Tests -GLU 024 -TSE 024 -GAG 024 -GPG 024 -PSE 024 -PRG 024 -HGL 024 -GAP 024 -HGLT 024 -HGL 024 -PGR 024 -HGLT 024 -EGC 024 -LTP 024 -GGLT 024 -GPG 024 -GSE 024 -LTP 024			
IDENTIFICATION = <i>Blast. capitatus</i>			
Clones	Probability	Strains	Contradictions
<i>Blast. capitatus</i>	99.87%	529	GLU [R]
<i>C. brassii</i>	0.12%	1649	LP [1]
Probability Level: Satisfactory Deficiency: Acceptable			
Test	<i>Blast. capitatus</i>	<i>C. brassii</i>	
Gelatin	+	+	36

Fig 4. Identification of Khamir using Electronic Rapid Compendium.

Isolates S310⁻¹ shows the results of ERIC web yeast identified species *Blastoschizomyces capitatus* with probability value of 99.87% presented in Figure 4. *B. capitatus* (otherwise known as *Geotrichum capitatum*) is capable of producing extracellular amylases. This yeast forms the basis for absorbing heavy metals in the production of amylases and fatty acids present in the waste (Falih, 1998).

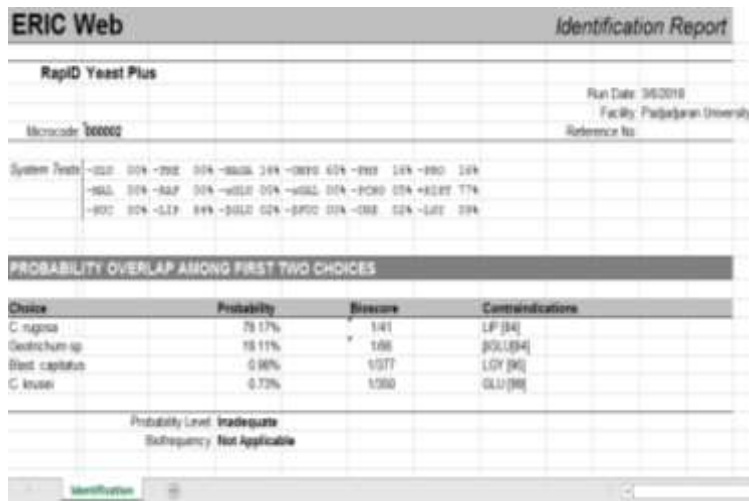


Fig 5. Identification of Khamir using Electronic Rapid Compendium.

The ERIC results in S310³ isolate showed that the identified species were *Candida rugosa* with a probability value of 79.17% which can be seen in Figure 5.

According Theerachat & Tanappong (2017), cultures of *C. rugosa* strains show the highest efficiency in COD reduction and high efficiency in triglyceride and degradation of phenolic compounds. Removal of COD by extracts of cell-free extracellular extracts is higher in palm oil water effluent.

Conclusion

Samples of textile waste were detected microorganisms are three species of yeast *Yarrowia lipolytica*, *Blastoschizomyces capitatus* and *Candida rugosa* which have the possibility of being able to process the best waste water.

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