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博 士 学 位 论 文

嗜碱细菌-真菌组合系统对印染废水的降解  
和脱色处理研究

Degradation and Decolorization of Textile Wastewater by a  
Combined System of Alkaliphile Bacteria and Fungi

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## 摘要

本研究针对印染废水染料脱色难助剂降解难两方面的问题展开微生物筛选和脱色处理研究。利用实验室已经获得的能够对多种染料高效降解的真菌菌群构建脱色反应系统,研究系统的脱色条件、脱色性能和稳定性;通过利用印染废水各工段的排水进行碱性条件下聚乙烯醇(PVA)降解菌群的富集筛选,并利用所获得的嗜碱细菌菌群构建嗜碱细菌-真菌集成脱色处理系统,在实验室小试和现场中试两个水平上研究集成系统对实际印染废水的处理效果,并结合传统微生物培养、电镜观察和现代分子生物学手段深入研究了筛选菌群在开放条件下对印染废水的适应性,为本研究进一步推广应用奠定基础。

构建了实验室规模的以真菌为主的染料脱色反应系统,实现了筛选微生物在开放条件下的长期优势生存并发挥脱色作用。用实验室前期获得的混合真菌菌群构建 4L 的生物膜反应器,对反应器运行条件的研究表明,外加碳源浓度对染料脱色率、矿化率、出水 pH 等起着重要的调控作用,提高葡萄糖浓度可以提高脱色率,但不利于染料的彻底矿化;适度的外加营养源可以保证高的矿化率和较好的水质。在葡萄糖浓度为 0.5 g/L 的情况下,对含有 30 mg/L 活性黑 5、活性红 M-3BE、酸性红 249 水样的脱色率达到 79%、68.7%、92.9%,矿化率达到 67.6%、51%和 90%,对色度为 200~320、COD 为 750~175 mg/L 的实际印染废水处理其色度和 COD 去除率均达到 90%左右。在反应器稳定运行的各阶段其生物膜上真菌细菌比例始终保持在 6.8:1~51.8:1 之间,说明系统中真菌菌群占绝对优势。在反应器连续开放条件下运行 3 个多月之后,对生物膜上的微生物菌群进行分子生物学分析,建立了细菌 16S rRNA 基因克隆文库和真菌 26S rRNA 基因克隆文库,通过对两个克隆文库进行序列相似性分析表明,细菌主要聚为四类,分别为 *Alphaproteobacteria*、*Betaproteobacteria*、*Gammaproteobacteria*、*Actinobacteria*。其中有 71.4%的序列属于 *Alphaproteobacteria*;真菌克隆文库中 70%的序列属于半知菌纲假丝酵母属,另外 26.7%聚在绿色木霉中。说明在真菌菌群中是以酵母菌为绝对优势真菌。

在印染废水助剂的降解方面,筛选获得了多组在碱性条件下(pH=8 和 pH=10)对实际印染废水不同工段中 PVA 和 COD 具有高降解能力的混合细菌菌群。

菌群对 PVA 浓度最高的退浆废水中 PVA 的去除率最高达到 66.7%，对 COD 的去除率最高达到 76.2%；利用所筛选的嗜碱性混合细菌成功构建了有效容积为 4L 的生物膜接触氧化反应器和 SBR 反应器，两种反应器均可以在碱性条件下对印染废水进行有效处理，生物膜接触氧化反应器的处理效果略高于 SBR 反应器。pH 为 10 的实际印染废水在 PVA 浓度 53~133 mg/L、COD 浓度 768~1112mg/L、色度 270~500 倍范围内波动时，经过水解酸化和嗜碱性生物膜接触氧化反应器处理后，PVA、COD、色度的去除率分别达到 50%~66.7%、70.4%~79.1%、15.8%~31.8%，并且 pH 下降到 8.8 左右。生物膜接触氧化反应器组合混合真菌脱色反应器之后，印染废水的 COD 不能得到进一步去除，但是色度可以进一步去除 40%~56.3%；利用分子生物学 PCR-DGGE 技术比较了各反应器在启动、运行中期和末期微生物群落的变化。在最初筛选的微生物菌群中只有约 34% 的细菌类群保留在反应器中；运行过程中，反应器类型和水质变化都对细菌菌群结构具有明显的影响；真菌反应器运行结束时，多数真菌类群被淘汰，只有 2 个种群明显存留在反应器生物膜上。

将小试的嗜碱细菌—真菌脱色处理系统进行扩大化，在河南荣祥纺织有限公司建立了“水解酸化—嗜碱细菌—真菌生物接触氧化—炉渣沙子过滤”中试工艺装置。中试进行了近 4 个月，在废水中 COD 为 330~1875 mg/L、色度为 100~500 倍范围内波动的情况下，COD 和色度去除率分别达到 91.2%和 95%，实现废水达标排放。系统稳定性好，易操作，抗各种染料成分变化的冲击力强。处理成本比目前广泛应用于印染行业的“水解酸化—生物接触氧化—混凝气浮”工艺每吨水节约处理费用 1.09 元。利用 PPM18S/T 膜分离装置进一步对中试沙滤出水直接进行纳滤深度处理，处理出水的各项指标达到印染行业工业用水的一级回用指标。

**关键词：**真菌菌群；嗜碱细菌；脱色反应系统；印染废水

## ABSTRACT

In this thesis, color decolorizing and additives degrading microorganisms were screened and textile wastewater treatment was studied aiming at the two difficult problems in the treatment of this kind of effluents. A decolorizing system with high efficiency was established using the fungal consortia obtained by the laboratory. The running conditions and process, working mechanism and decolorization performance of the system were investigated in detail. A group of alkaliphile microbial consortium was obtained after enriching and screening using the effluents from every process of dyeing and printing. An integrated system of alkaliphile bacteria and fungi reactors was established to assess the textile wastewater treatment performances by selected microbial consortia under lab-scale and pilot tests in site. Various microbial community analysis methods including traditional cultivation, electron microscopic observation and molecular biological techniques were applied to evaluate the adaptability of the above microbial consortia to the textile wastewater.

A decolorizing eco-system which was dominant with the obtained fungi was successfully established. It was a breakthrough that the system could run under open conditions with the screened microorganisms dominantly surviving for a long time. Study results for the system running parameters indicated that the nutrition concentrations had a great influence to the decolorization and mineralization rates, the effluents pH and SS, etc. Increase of the glucose concentration in the influents could significantly improve the color removal efficiency, but was not helpful for dye mineralization. Adding a suitable proportion of nutrients in the influents could ensure an ideal effluents' characteristic. For the decolorization of reactive black5, reactive red M-3BE and acid red 249, color removal rate of 79%, 68.7%, 92.9% and dye mineralization of 67.6%, 51%, 90% were respectively obtained under the condition of 0.5 g/L glucose supplemented in the influents. For the treatment of real textile wastewater, about 90% removal rate of COD and chroma under the condition of 0.2g/L glucose fed even when the influent COD and chroma were changed within

750~1175mg/L and 200~320 respectively. During the whole running course of bioreactor, the microbial community was monitored. The ratio of fungi to bacteria was kept at 6.8:1~51.8:1 suggesting an absolute dominant position of fungi in the system. Further analysis of microbial community was conducted by constructing 16S rRNA and 26S rRNA clone libraries. The results showed that all bacterial clones were clustered in 4 groups: *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Actinobacteria* with the majority of *Alphaproteobacteria* (71.4%) in the system and all the fungal clones were clustered in genera of *Candida* and *Trichoderma* with 70% of *Candida.spp* and 26.7% of *Trichoderma viride*. It was obvious that yeasts were the predominant fungi in the system even after 4 months running under open conditions.

For degradation of additives in the textile wastewater, a few groups of alkaliphile bacteria consortim with high efficiencies of degrading PVA and COD were obtained by screening using effluents from different dyeing and printing processes. The highest removal rate of PVA and COD to the strongest effluents from desizing process was 66.7% and 76.2%, respectively. Two bioreactors (biological contact oxidation and SBR) were established using the obtained alkaliphile microbial consortia to compare which was more suitable for such wastewater treatment and the screened microorganisms conservation in the system. The former was a bit better than the latter. Under the influents conditions of pH10, PVA 53~133 mg/L, COD 768~1112 mg/L, colority 270~500 dilutions, the PVA, COD and color removal rate reached 50%~66.7%, 70.4%~79.1% and 15.8%~31.8%, respectively after hydrolytic acidification and alkaliphile bacteria treatment. The effluents pH declined to 8.8. Unlike the COD, the color could be further removed 40%~56.3% when integrated a fungi decolorizing system after the alkaliphile reactor. The final effluents could be up to the national standards after a simple flocculation and sedimentation process. Variation of the microbial community was monitored in the above bioreactors in every stage, such as starting, middle running and the end by comparing the bands profile in the PCR-DGGE gel. The results indicated that only 34% species of microorganisms in the initial consortium were conserved in the bioreactors. There was significant



influence of the type of bioreactor and the variation of the influents on the microbial community structure. Most species of fungi were lost and only 2 species became the dominant population after running for near two months.

An integrated pilot textile wastewater process “hydrolytic acidification-alkaliphile bacteria-fungal contact oxidation-slag sand filtration” was established in Henan Rongxiang Textile Limited Company by enlarging the lab-scale system. The integrated system ran for 4 months and could remove 91.2% COD and 95% chroma of the wastewater under the influents conditions of COD 330~1875 mg/L and chroma 100~500 dilutions. The treated effluents were up to the discharging standards. The integrated system exhibited very good application prospects due to its high stability, easy operability and high resistance to various wastewater characteristics. The cost of our treatment process was lower about 1.09 RM Yuan than the current widely used process “hydrolytic acidification-contact oxidation-coagulation floatation”. For the effluents from the above process, further deep treatment was conducted using nanofiltration technique. The results indicated that the various indexes of the treated water were up to the reuse standards for textile industry.

**KEY WORDS:** Fungal consortium; Alkaliphile bacteria and fungi; Decolorizing system; Textile wastewater.

# 目录

摘要 .....	I
ABSTRACT .....	III
<b>第一章 绪论 .....</b>	<b>1</b>
§ 1.1 染料的结构、分类及对环境的危害 .....	1
§ 1.2 我国染料废水污染现状 .....	2
§ 1.3 印染废水的来源、水质特点 .....	3
1.3.1 印染废水的来源 .....	3
1.3.2 印染废水的水质特点 .....	3
§ 1.4 印染废水处理办法 .....	5
1.4.1 物理法 .....	5
1.4.2 化学法 .....	8
1.4.3 生物法 .....	12
§ 1.5 染料的生物脱色研究进展 .....	16
1.5.1 真菌对染料的脱色研究 .....	17
1.5.2 细菌对染料的脱色研究 .....	21
1.5.3 藻类对染料的脱色研究 .....	22
1.5.4 混合菌群 .....	22
§ 1.6 嗜碱微生物及其在废水处理中的应用 .....	23
1.6.1 嗜碱微生物简介 .....	23
1.6.2 嗜碱微生物的嗜碱机理 .....	25
1.6.3 嗜碱微生物在废水处理方面的应用 .....	26
§ 1.7 聚乙烯醇 (PVA) 在纺织印染中的应用、污染和生物降解 .....	28
1.7.1 聚乙烯醇简介 .....	28
1.7.2 聚乙烯醇的生物降解机理 .....	29
1.7.3 降解聚乙烯醇的微生物 .....	31
§ 1.8 污水处理系统中微生物生态群落分析新技术 .....	36
§ 1.9 本研究的目的是、意义和课题的提出 .....	37
§ 1.10 论文设想 .....	39
<b>第二章 脱色真菌反应系统的构建和微生物群落组成分析 .....</b>	<b>41</b>
§ 2.1 材料和方法 .....	43
2.1.1 培养基 .....	43
2.1.2 高效脱色混合真菌培养液 .....	43
2.1.3 染料 .....	44
2.1.4 主要试剂及溶液配制 .....	45
2.1.5 主要实验仪器 .....	45
2.1.6 人工配制染料废水 .....	45
2.1.7 实际印染废水 .....	46
2.1.8 脱色率计算方法 .....	46

2.1.9 酶活性测定方法及酶单位定义 .....	46
2.1.10 水质分析项目和方法 .....	47
2.1.11 连续小试装置和操作条件 .....	47
2.1.12 反应器中优势微生物菌群的生物培养.....	48
2.1.13 生物膜上微生物群落基因组 DNA 的提取 .....	49
2.1.14 细菌 16S rRNA 和真菌 26S rRNA 基因扩增.....	49
2.1.15 PCR 产物的克隆和转化.....	49
2.1.16 测序和序列分析 .....	50
<b>§ 2.2 结果与讨论 .....</b>	<b>50</b>
2.2.1 真菌连续脱色系统的构建和脱色条件研究.....	50
2.2.2 真菌连续脱色系统对其他染料的脱色能力.....	55
2.2.3 真菌连续脱色系统对实际印染废水的处理.....	56
2.2.4 真菌反应器中脱色菌群的产酶分析 .....	57
2.2.5 真菌反应器中脱色菌群的生物培养计数分析.....	57
2.2.6 真菌反应系统中微生物群落的分子生物学解析.....	59
<b>§ 2.3 本章小结 .....</b>	<b>65</b>
<b>第三章 嗜碱性 PVA 降解细菌的筛选和降解性能研究.....</b>	<b>67</b>
<b>§ 3.1 材料与方法 .....</b>	<b>67</b>
3.1.1 样品来源 .....	67
3.1.2 培养基 .....	68
3.1.3 富集与驯化 .....	68
3.1.4 分析项目与测定方法 .....	68
<b>§ 3.2 结果与分析 .....</b>	<b>69</b>
3.2.1 pH=8 时不同菌源对废水中 PVA 和 COD 的去处效果 .....	69
3.2.2 pH=10 时不同菌源对废水中 PVA 和 COD 的去处效果 .....	71
3.2.3 单菌株对实际废水中 PVA 的降解效果 .....	73
<b>§ 3.3 本章小结 .....</b>	<b>76</b>
<b>第四章 印染废水嗜碱细菌—真菌集成脱色处理 系统的构建和小试运行..</b>	<b>77</b>
<b>§ 4.1 前言 .....</b>	<b>77</b>
<b>§ 4.2 材料与方法 .....</b>	<b>78</b>
4.2.1 小试所用印染废水水质 .....	78
4.2.2 小试工艺流程 .....	78
4.2.3 印染废水小试反应器的构建 .....	79
4.2.4 反应器中微生物群落分析 .....	80
4.2.5 显微镜观察 .....	80
<b>§ 4.3 结果与讨论 .....</b>	<b>81</b>
4.3.1 水解酸化反应器对实际印染废水的处理效果.....	81
4.3.2 嗜碱性生物反应器对实际印染废水的处理效果.....	83
4.3.3 真菌脱色反应器对实际印染废水进一步的脱色处理.....	86
4.3.4 嗜碱细菌—真菌集成处理系统对印染废水中污染物的总处理效果.....	87
4.3.5 嗜碱细菌—真菌脱色处理系统中微生物群落组成分析.....	89
<b>§ 4.4 本章小结 .....</b>	<b>93</b>

<b>第五章 实际印染废水的中试处理研究</b> .....	<b>95</b>
§ 5.1 材料和方法 .....	<b>95</b>
5.1.1 河南荣祥织染有限公司印染工艺 .....	95
5.1.2 废水水样来源 .....	95
5.1.3 废水水样水质特征 .....	96
5.1.4 原有污水处理工艺、效果及存在的问题 .....	97
5.1.5 嗜碱细菌-真菌集成脱色处理系统印染废水处理中试工艺流程 .....	97
§ 5.2 嗜碱细菌-真菌集成脱色系统处理印染废水中试研究结果 .....	<b>98</b>
5.2.1 中试反应系统的建立 .....	98
5.2.2 水解酸化池的运行效果评价 .....	98
5.2.3 嗜碱细菌-真菌集成处理系统的运行效果 .....	100
5.2.4 炉渣-石英砂对集成反应系统出水的过滤作用 .....	102
§ 5.3 印染废水生化处理出水的深度处理初探 .....	<b>105</b>
5.3.1 二级印染废水处理技术的局限性 .....	105
5.3.2 纳滤膜技术的应用和印染废水深度处理 .....	106
5.3.3 实验结果 .....	107
§ 5.4 经济效益分析 .....	<b>109</b>
5.4.1 嗜碱细菌-真菌脱色处理工艺处理印染废水达标排放的经济效益分析 .....	109
5.4.2 印染废水“嗜碱细菌-真菌处理+深度处理回用”的经济效益分析 .....	110
§ 5.5 印染废水“嗜碱细菌-真菌处理+深度处理回用”的环境效益分析 .....	<b>111</b>
§ 5.6 本章小结 .....	<b>111</b>
<b>第六章 总结与展望</b> .....	<b>113</b>
§ 6.1 主要结论 .....	<b>113</b>
§ 6.2 研究展望与建议 .....	<b>115</b>
参考文献 .....	<b>116</b>
博士学习期间发表的论文和科研成果 .....	<b>132</b>
致谢 .....	<b>133</b>

# Table of Contents

<b>ABSTRACT IN CHINESE .....</b>	<b>I</b>
<b>ABSTRACT IN ENGLISH .....</b>	<b>III</b>
<b>Chapter 1 Introduction.....</b>	<b>1</b>
§ 1.1 Dyes' structures, classification and danger to environments .....	1
§ 1.2 Current pollution status in China by dye containing wastewater .....	2
§ 1.3 Sources and characteristics of textile wastewater .....	3
1.3.1 Sources of textile wastewater .....	3
1.3.2 Characteristics of textile wastewater .....	3
§ 1.4 Treatment methods of Textile wastewater .....	5
1.4.1 Physical methods .....	5
1.4.2 Chemical methods .....	8
1.4.3 Biological methods .....	12
§ 1.5 Current research development on dyes' biological decolorization .....	16
1.5.1 Dye decolorization by fungi .....	17
1.5.2 Dye decolorization by bacteria .....	21
1.5.3 Dye decolorization by algae .....	22
1.5.4 Dye decolorization by mixed microbial consortium.....	22
§ 1.6 Alkalophile and their application in wastewater treatment.....	23
1.6.1 Introduction of alkalophile.....	23
1.6.2 Alkalophile mechanism for alkaline .....	25
1.6.3 Application of alkalophile in wastewater .....	26
§ 1.7 Application, pollution and biodegradation of polyvinyl in textile industry.....	28
1.7.1 Introduction of polyvinyl.....	28
1.7.2 Mechanism for polyvinyl's biodegradation .....	29
1.7.3 Microbes which could degrade polyvinyl.....	31
§ 1.8 New techniques for micro-ecology analysis in wastewater treatment system.....	36
§ 1.9 Targets and importance of this study .....	37
§ 1.10 Assumed dissertation .....	39
<b>Chapter 2 Establishment of decolorizing fungi system and microbial community analysis.....</b>	<b>41</b>
§ 2.1 Materials and methods .....	43
2.1.1 Culturing medium.....	43
2.1.2 Medium for mixed fungi with high performance of decolorization .....	43
2.1.3 Dyes .....	44
2.1.4 Main reagents and solution preparation.....	45
2.1.5 Main test instruments.....	45
2.1.6 Artificial dye wastewater .....	45
2.1.7 Real dye wastewater .....	46

2.1.8	Calculation methods for decolorization rate .....	46
2.1.9	Measurement methods for enzyme activities and definition for enzyme units....	46
2.1.10	Analysis items and methods for wastewater characteristics .....	47
2.1.11	Continuous lab-scale equipments and operation conditions .....	47
2.1.12	Cultivation of dominant microbes in bioreactors.....	48
2.1.13	Extraction of total genome DNA on biofilm.....	49
2.1.14	Gene amplification of bacterial 16S rRNA and fungal 26S rRNA .....	49
2.1.15	Clone and trasformation of PCR products .....	49
2.1.16	Sequencing and analysis .....	50
<b>§ 2.2</b>	<b>Results and discussion .....</b>	<b>50</b>
2.2.1	Establishment of decolorizing fungi system and decolorization conditions.....	50
2.2.2	Decolorization performance on other dyes by fungal decolorizing system.....	55
2.2.3	Treatment of real textile wastewater by fungal decolorizing system.....	56
2.2.4	Enzyme production by decolorizing consortium in fungal reactor .....	57
2.2.5	Cultivation and enumeration of decolorizing microbes in the fungi reactor .....	57
2.2.6	Molecular biological analysis of microbial community in the fungi reactor .....	59
<b>§ 2.3</b>	<b>Summary.....</b>	<b>65</b>
<b>Chapter 3</b>	<b>Screening and performance of PVA degradating alkalophile .....</b>	<b>67</b>
<b>§ 3.1</b>	<b>Materials and methods .....</b>	<b>67</b>
3.1.1	Samples.....	67
3.1.2	Medium.....	68
3.1.3	Enrichment and acclimation .....	68
3.1.4	Analysis items and methods .....	68
<b>§ 3.2</b>	<b>Results and discussion .....</b>	<b>69</b>
3.2.1	PVA and COD removal effects in wastewater under condition of pH 8 .....	69
3.2.2	PVA and COD removal effects in wastewater under condition of pH 10 .....	71
3.2.3	PVA degradation effects in wastewater by pure microbial strains.....	73
<b>§ 3.3</b>	<b>Summary.....</b>	<b>76</b>
<b>Chapter 4</b>	<b>Establishment and operation of alkalophile-fungi integrated decolorizing system for textile wastewater .....</b>	<b>77</b>
<b>§ 4.1</b>	<b>Introduction.....</b>	<b>77</b>
<b>§ 4.2</b>	<b>Materials and methods .....</b>	<b>78</b>
4.2.1	Characteristics of wastewater in lab-scale test.....	78
4.2.2	Process chart for lab-scale test.....	78
4.2.3	Establishment of lab-scale reactor for textile wastewater.....	79
4.2.4	Analysis of microbial community in reactor .....	80
4.2.5	Observation of microbes by microscope.....	80
<b>§ 4.3</b>	<b>Results and discussion .....</b>	<b>81</b>
4.3.1	Treatment effects of textile wastewater by hydrolytic acidification unit.....	81
4.3.2	Treatment effects of textile wastewater by alkalophile reactor.....	83
4.3.3	Further decolorization treatment by fungal reactor.....	86
4.3.4	Total treatment effects of textile wastewater by alkalophile-fungi integrated system.....	87

4.3.5	Analysis of microbial community in alkalophile-fungi integrated system .....	89
§ 4.4	Summary.....	93
<b>Chapter 5</b>	<b>Pilot test study on real textile wastewater treatment.....</b>	<b>95</b>
§ 5.1	<b>Materials and methods .....</b>	<b>95</b>
5.1.1	Production process in Henan Rongxiang Printing and Dyeing Co. Ltd .....	95
5.1.2	Wastewater resource .....	95
5.1.3	Characteristics of wastewater .....	96
5.1.4	Original wastewater treatment process, effects and problems .....	97
5.1.5	Pilot test process of wastewater treatment using alkalophile-fungi integrated system.....	97
§ 5.2	<b>Pilot treatment results of textile wastewater using alkalophile-fungi integrated system .....</b>	<b>98</b>
5.2.1	Establishment of pilot treatment system.....	98
5.2.2	Running effects of hydroacidification unit .....	98
5.2.3	Running effects of alkalophile-fungi integrated system .....	100
5.2.4	Filtration effects of effluents from the integrated system by slag-sand .....	102
§ 5.3	<b>Primary study on advanced treatment of textile effluents from biochemical treatment.....</b>	<b>105</b>
5.3.1	Limitation of two-stage textile wastewater treatment techniques.....	105
5.3.2	Application of nanofiltration membrane and advanced treatment of textile wastewater .....	106
5.3.3	Results .....	107
§ 5.4	<b>Analysis of economic benefits.....</b>	<b>109</b>
5.4.1	Analysis of economic benefits for emission on standard using alkalophile-fungi integrated textile wastewater treatment process .....	109
5.4.2	Analysis of economic benefits for “alkalophile-fungi integrated textile wastewater treatment + advanced treatment and reuse” process.....	110
§ 5.5	<b>Analysis of environmental benefits for “alkalophile-fungi integrated textile wastewater treatment + advanced treatment and reuse” process.....</b>	<b>111</b>
§ 5.6	Summary.....	111
<b>Chapter 6</b>	<b>Summary and Prospect .....</b>	<b>113</b>
§ 6.1	Main conclusion .....	113
§ 6.2	Research prospect and suggestion .....	113
<b>References.....</b>		<b>116</b>
<b>Published papers and achievements during PhD study .....</b>		<b>132</b>
<b>Acknowledgements .....</b>		<b>133</b>

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