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Travaux pratiques – Galaxy* (partie 4)

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* Les captures d'écran ont été réalisées en 2022, il est possible que l'interface aujourd'hui soit légèrement différente.

Etape 1 : Connexion à Galaxy

- Se connecter à l'instance Galaxy « France » : <u>https://usegalaxy.fr/</u>
- Créer un nouvel historique de travail

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Données utilisées pour le TP

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Article

Characterization of the Radiation Desiccation Response Regulon of the Radioresistant Bacterium *Deinococcus radiodurans* by Integrative Genomic Analyses

Nicolas Eugénie ⁽⁰⁾, Yvan Zivanovic ⁽⁰⁾, Gaelle Lelandais, Geneviève Coste, Claire Bouthier de la Tour, Esma Bentchikou, Pascale Servant [†] and Fabrice Confalonieri ^{*,†}

RNA-seq; bioinformatic analyses

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Abstract: Numerous genes are overexpressed in the radioresistant bacterium Deinococcus radiodurans

after exposure to radiation or prolonged desiccation. It was shown that the DdrO and IrrE proteins play a major role in regulating the expression of approximately twenty genes. The transcriptional

repressor DdrO blocks the expression of these genes under normal growth conditions. After exposure

to genotoxic agents, the IrrE metalloprotease cleaves DdrO and relieves gene repression. At present,

many questions remain, such as the number of genes regulated by DdrO. Here, we present the first

ChIP-seq analysis performed at the genome level in Deinococcus species coupled with RNA-seq, which

was achieved in the presence or not of DdrO. We also resequenced our laboratory stock strain of D.

radiodurans R1 ATCC 13939 to obtain an accurate reference for read alignments and gene expression

quantifications. We highlighted genes that are directly under the control of this transcriptional

repressor and showed that the DdrO regulon in D. radiodurans includes numerous other genes than

those previously described, including DNA and RNA metabolism proteins. These results thus pave

the way to better understand the radioresistance pathways encoded by this bacterium and to compare

Keywords: radioresistance/desiccation; transcriptional regulator; Deinococcus radiodurans; ChIP-seq;

the stress-induced responses mediated by this pair of proteins in diverse bacteria.

check for updates

Clustions: Engénico, N., Z. Kavarovic, Y.; Lelandaris, G.; Coste, G.; Bouthier de Bioru, C.; Berkhälkou, E.; Servand, P.; Confalomeri, F. Characterization of the Radiation Desizeation Response Regular on the Radiaconsistant Backeriann Driftocencer and/advances Integrative Genomic Analyses. *Cells* 2021, 10, 2506. https://doi.org/ 10.3309/cells102056

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Copyright © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). 1. Introduction Deinococcus radiodurans is one of the most resistant bacteria to genotoxic agent exposure and desiccation isolated to date [1–4]. Unlike radiosensitive organisms, once exposed to huge y-ray doses, or after prolonged desiccation, *D. radiodurans* is able to reconstruct an intact genome in a few hours from several hundred DNA fragments [5]. Many factors contribute to the radioresistance of *D. radiodurans*, including efficient DNA repair mech-anisms [5–8], a condensed nucleoid limiting the dispersion of genome fragments after irradiation [9,10], and the protection of proteins against oxidative damage [11]. Thus, the exceptional ability of this bacterium to overcome severe DNA damaging conditions is described as a combination of active and passive mechanisms acting in synergy within the cell, enabling survival following these stresses.

The exposure of *D. radiodurans* to γ -rays, or its recovery from desiccation, results in a rapid upregulation of the expression of numerous genes [12,13], even if constitutively expressed genes are also involved in the mechanisms of radioresistance. In many bacterial species, expression of DNA repair genes is under the control of LexA, the repressor of the well-known SOS response (for review [14]). *D. radiodurans* encodes two LexA homologs

Cells 2021, 10, 2536. https://doi.org/10.3390/cells10102536

https://www.mdpi.com/journal/cells





Etape 2 : Importer les résultats des comptages (TP3)

Récupérer dans votre nouvel historique de travail la collection des fichiers TXT :



Etape 2 : Importer les résultats des comptages (TP3)

 Vérifier le contenu de la collection, les résultats pour les 6 échantillons suivant doivent être présents :

Run	Assay Type	strain	treatment	type-material	time_point
SRR14698434	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	1H
SRR14698435	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	1H
SRR14698436	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	1H
SRR14698437	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	4H
SRR14698438	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	4H
SRR14698439	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	4H

Etape 3 : Simplification des noms de fichiers

• Pour faciliter l'utilisation de DESeq2, renommer les fichiers par conditions (1H00 et 4H00) :

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featureCounts Measure gene expression in RNA-Seq experiments from SAM or BAM files.	Specify a factor level, typical values could be 'tumor', 'normal', 'treated' or 'control' 4H00		
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FROGSSTAT DESeq2 Preprocess import a Phyloseq object and prepare it for DESeq2 differential abundance analysis			Curron	X	
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Etape 5 : Partager l'historique des résultats



Fin de la partie 4 ^(C)



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Gaëlle LELANDAIS

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