セミナーのお知らせ

From metabolism and epigenetics: safeguarding the genome

講演者　Dr. Susan M. Gasser

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Professor of Molecular Biology, University of Basel

日　時：10月12日（木）15:00~16:15

場　所：東京大学農学部２号館 化学第３教室
（参加費・事前申し込み不要）

Histone H3K9 methylation is a conserved modification that correlates broadly with gene repression in organisms ranging from fission yeast to man. In *C. elegans*, di- and tri-K9 methylation is abundant on repetitive elements (RE), including both transposons and simple repeats, and coats both pseudogenes and silent tissue-specific genes. Using a double mutant that eliminates the two *C. elegans* H3K9 histone methyltransferases, SET-25 and MET-2, we find that H3K9me is dispensable for development[1], although worms become ts sterile. This correlates with extensive DNA damage-driven apoptosis in the germline, without elevated mitotic or meiotic chromosome missegregation. Instead, we find that the loss of H3K9methylation leads to the promiscuous and widespread expression of all classes of repetitive elements (DNA and RNA transposons, and simple repeats) in both germline and somatic tissues. The loss of transcriptional silencing correlates with an accumulation of insertions and deletions at repetitive sequences, and renders worms sensitive to replication fork stalling, but not ionizing radiation. RNA-DNA hybrids accumulate in the absence of H3K9me even without exogenous stress, which is exacerbated by the loss of the C. elegans BRCA1 complex, specifically at tandem repeats and not at RNA or DNA transposons. We conclude that a key function of H3K9me is to ensure the stability of a repeat-rich genome, most specifically by suppressing the transcription of simple repeats. Intriguingly, impaired metabolism and mutation of NAD-dependent histone deacetylases also leads to a loss of H3K9 methylation and provokes a similar loss of genome stability. This links impaired metabolism, such as that which accumulates in ageing organisms, with repeat-based expression and transposon activation.

[1]Zeller, P., Padeken, J., van Schendel, R., Kalck, V., Tijsterman, M. and Gasser, S.M. (2016) Histone H3K9 methylation is dispensable for *C. elegans* development, but suppresses RNA-DNA hybrid-associated repeat instability. **Nature Genetics**, *48*, 1385 - 1395. doi: 10.1038/ng.3672

Dr. Susan M. Gasser ご略歴：
Professor of Molecular Biology, University of Basel
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Research Focus: epigenetics, genome mapping, yeast genetics, stem cells, nuclear aspects of gene expression, cell plasticity
Member of the European Commission Advisory Group on Health Research
Awards:
INSERM International Prize (2011)
FEBS | EMBO Women in Science Award (2012)
Women in Science award (2013)

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Dr. Susan M. Gasser による
男女共同参画のための講演会

演題

「Women in Science: the challenges in Europe」

日時：平成29年10月12日（木）16:30～17:30
場所：東京大学農学部２号館　１階　化学第３教室
（http://www.u-tokyo.ac.jp/campusmap/cam01_07_02_j.html）
定員：なし（事前登録不要 .どなたでも参加できます.）

女性のみならず男性の参加も歓迎しております。
この機会にぜひご参加ください。

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問い合わせ先：東京大学大学院農学生命科学研究科応用生命化学専攻
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Seminar for Gender Equality
by Dr. Susan M. Gasser

“Women in Science: the challenges in Europe”

Oct. 12（Thu）16:30～17:30
Venue : Yayoi Campus, Agri.Bldg.2　1 F
Chemistry Third Classroom
(http://www.a.u-tokyo.ac.jp/english/campus/map-e.html#3)

No reservation needed.
Please come to join us whether you are man or woman.

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