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Evaluation of neutron spectrum for pin-by-pin MA transmutation analysis by reconstruction of neutron flux distribution

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Abstract - *Pin-by-pin MA transmutation is analyzed by proposed method which is based on the reconstruction of neutron flux distribution in heterogeneous MA target loaded core. The distribution of pin-by-pin transmutation is steep in the core since MA target assembly contains Zirconium-hydride rod for efficient transmutation. Proposed method reveals the detailed distribution of pin-by-pin MA transmutation for each nuclide. As for total amount of MA transmutation in the core, the difference between proposed method and homogenization method is not remarkable.*

I. INTRODUCTION

Minor actinides (MAs) remain within high level radioactive wastes created by nuclear reprocessing and have radiotoxicity over the long term. For effective reduction of MAs, Partitioning and Transmutation strategies have been compared and discussed. The most prospective approach to reduce MAs is based on the introduction of fast reactors [1]. Fast reactors can be classified by its coolant because the design parameters such as system power depend on coolant. However, the transmutation physics behavior is not different basically [2].

On the other hand, a concept of sodium cooled fast reactor designed for efficient transmutation of MA has been proposed by Fujimura et al. [3]. This reactor employs MA target assemblies composed of MA rod and solid moderator. The study shows zirconium-hydride is optimum moderator for the improvement of MA transmutation. Using the Zirconium-hydride rod, another fast reactor core which can achieve large amount of MA transmutation is designed [4].

In the MA assembly which contains moderator rod, the neutron spectrum varies depending on the location of fuel pin. This indicates that rigorous analysis of the amount of MA transmutation needs rigorous evaluation considering its heterogeneity. Whole core pin-by-pin calculation can directly solve the pin-by-pin neutron spectrum which is needed for accurate evaluation of MA transmutation. However, the computational cost of this detailed calculation is not negligible even taking into account the rapid improvements in computational abilities.

An approach solving detailed neutron spectrum without huge computational costs is introducing multi-group nodal method. Multi-group nodal method is widely used and studied by many researchers [5, 6]. One of recent works about multi-group nodal method is focused on improvement of the pin power accuracy in complex core which contains UO_2 and MOX assemblies [7]. Including this work, multi-group nodal method is developed in order to enhance the accuracy of the pin power and is not aimed for the neutron spectrum which is necessary for detailed evaluation of transmutation.

In this paper, the calculation scheme which can evaluate the neutron spectrum for accurate analysis of pin-by-pin MA transmutation is proposed. In the following section, target fast reactor core, calculation scheme, and the result of MA transmutation are described.

II. TARGET FAST REACTOR CORE

The target fast reactor core is shown in Fig. 1, This 750 MWe core is composed of 232 inner fuel assemblies, 165 outer fuel assemblies and 84 heterogeneous MA target assemblies (Fig. 2). The weight ratio of MA in MA target fuel is 15.3 wt%. The composition of MA is shown in Table I.

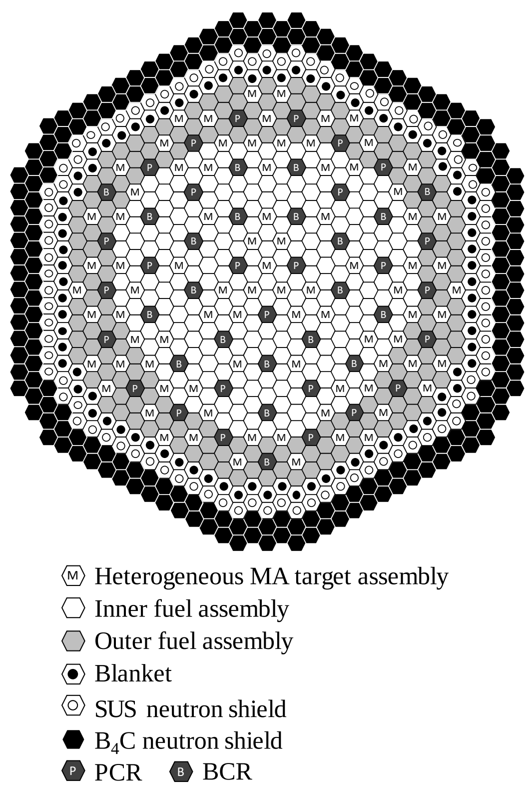


Fig. 1. Heterogeneous MA target loaded core

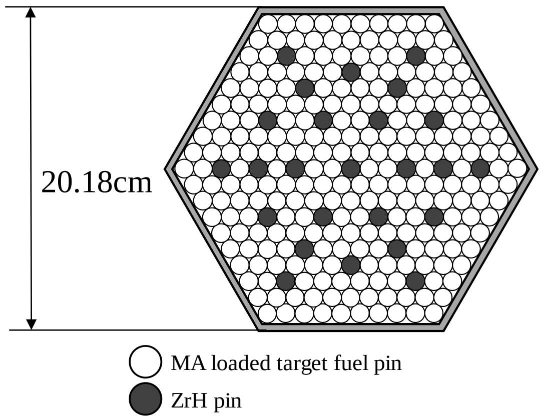


Fig. 2. Heterogeneous MA target assembly

As shown in Fig. 1, the MA target assembly is surrounded by inner fuel assemblies. Therefore, neutron flux distribution generally shows parabolic shape (Fig. 3).

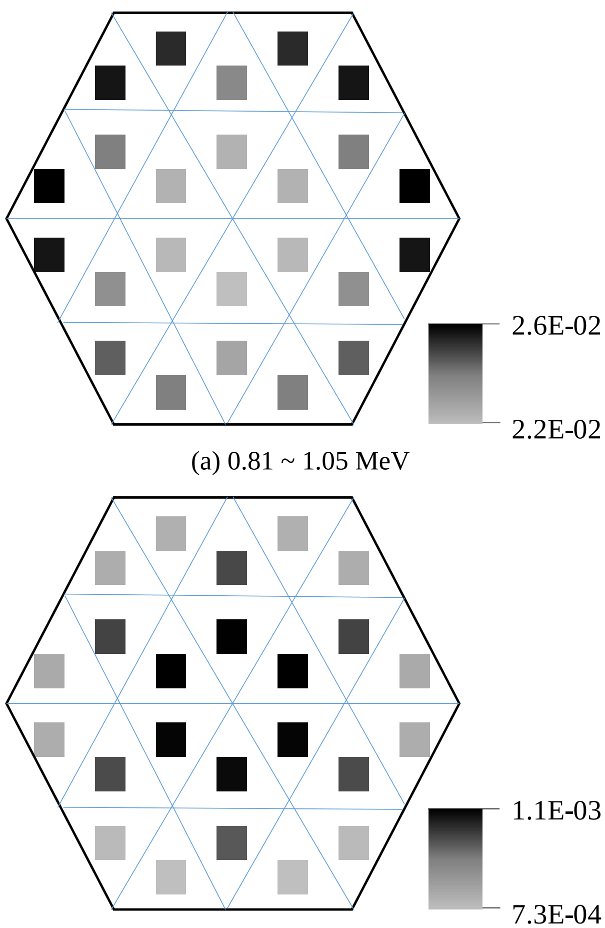


Fig. 3. Neutron flux distribution in MA target assembly

Table I. Composition of loaded MA

Np-237	0.66
Np-239	0.04
Am-241	70.46
Am-242m	2.99
Am-243	14.82
Cm-242	2.13
Cm-243	0.28
Cm-244	7.13
Cm-245	1.28
Cm-246	0.20
Cm-247	0.01

[wt%]

III. CALCUATION SCHEME

The calculation scheme compared by traditional core analysis is shown in Fig. 4. As shown in Fig. 4, pin-by-pin neutron spectrum is evaluated by the reconstructed neutron fluxes obtained from the assembly calculation and the core calculation without energy collapse. Therefore, the burnup calculation is performed by pin-by-pin neutron spectrum by proposed method. In this study, 70-group assembly calculation is carried out by MOC code BACH [8] by using the cross section based on JENDL-4.0, and two dimensional core calculation is carried out by diffusion calculation code CITATION [9]. The number of mesh division of an assembly is fixed to 24 at core calculation. The burnup calculation is performed by ORIGEN2 by replacing the one group cross section [10].

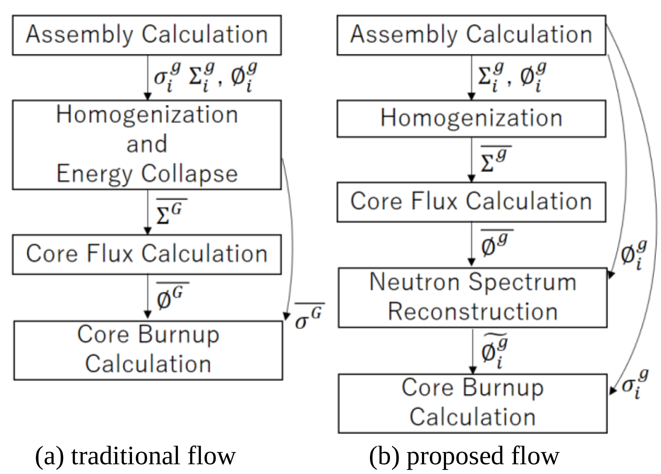
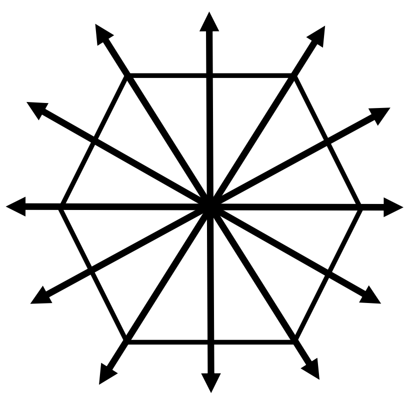


Fig. 4. Comparison of calculation flow

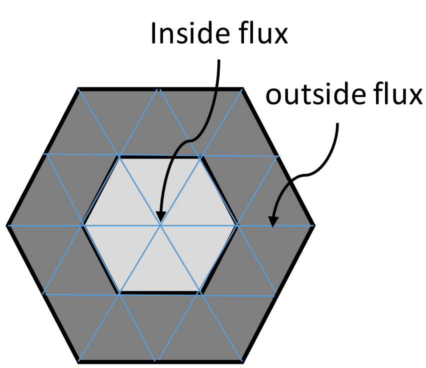
Pin-by-pin neutron flux $\widetilde{\phi_{i,sa}^g}$ is reconstructed as

$$\widetilde{\phi_{i,sa}^g} = \phi_{i,sa}^g \times (1 + ar^2 + bx_1 + cx_2 + \alpha)_g \times \frac{\overline{\phi_{core}^g}}{\overline{\phi_{sa}^g}}, \quad (1)$$

where $\emptyset^g_{i,sa}$ is the neutron flux obtained by assembly calculation and $\overline{\emptyset^g_{core}}$ is the neutron flux obtained by core calculation and $(1 + ar^2 + bx_1 + cx_2 + \alpha)_g$ is correction term which takes the flux distribution obtained by the core calculation into account. The correction them can be classified into linier correction term and quadric correction term. Linier correction term $(bx_1 + cx_2)$ is defined by two coordinate (x_1, x_2) and their coefficients (b, c). Coefficients b and c are defined from two of the twelve directions shown in Fig. 5 (a). The coefficient b is the sharpest neutron flux gradient in directions shown in Fig. 5 (a) and the other coefficient c is neutron flux gradient in the orthogonal direction. x_1 and x_2 are coordinate of directions chosen by b and c, respectively. Quadric correction term $(ar^2 + \alpha)$ is defined by three parameters (r, a, α). r is the distance from the center of assembly, and a is the coefficient of r^2, and α is a parameter which normalizes the average flux of the assembly. As is shown in Fig. 3, the shape of the neutron distribution in MA target assembly is generally parabolic. Therefore, the term ar^2 is introduced in order to describe parabolic shape in an assembly by using inside flux and outside flux (Fig. 5 (b)).



(a) direction for linear correction term



(b) inside flux and outside flux for quadric correction term

Fig. 5. Definitions for reconstruction

The normalization parameter α is easily derived by solving following equation.

$$\sum_i\left(\left(\emptyset^g_{i,sa} \times (1 + ar^2 + bx_1 + cx_2 + \alpha) \times \frac{\overline{\emptyset^g_{core}}}{\overline{\emptyset^g_{sa}}}\right) \times V_i\right) = \sum_i\left(\left(\emptyset^g_{i,sa} \times \frac{\overline{\emptyset^g_{core}}}{\overline{\emptyset^g_{sa}}}\right) \times V_i\right). \quad (2)$$

In Eq. (2), $\sum_i\left(b\emptyset^g_{i,sa}x_1V_i\right)$ and $\sum_i\left(c\emptyset^g_{i,sa}x_2V_i\right)$ is zero because these terms are the odd function. Then, α is expressed as

$$\alpha = -a\sum_i\left(\emptyset^g_{i,sa}r^2V_i\right)/\sum_i\left(\emptyset^g_{i,sa}V_i\right). \quad (3)$$

IV. RESULTS

The calculation results are compared with the results obtained from 70-group CITATION calculation without the proposed reconstruction of the neutron flux. The neutron spectrum and the amount of MA transmutation are shown in this section.

Figure 6 shows the location where the calculation results compared in. Figure 7 shows the comparison of the neutron spectrum. It is found that the neutron spectrum of CITATION is softer than reconstructed result because CITATION calculation uses assembly-wise homogenized cross-section which includes zirconium-hydride rods. Figures 8-12 show pin-by-pin transmutation of each nuclide. These results show that shape of pin-by-pin transmutation depends on the nuclide and pin-by-pin distribution of MA transmutation is evaluated by reconstruction. On the other hand, the total MA transmutation in an MA assembly results in almost the same amount of CITATION result as shown in Fig. 13. A similar tendency is seen in total MA transmutation in all MA assembly as shown in Fig. 14.

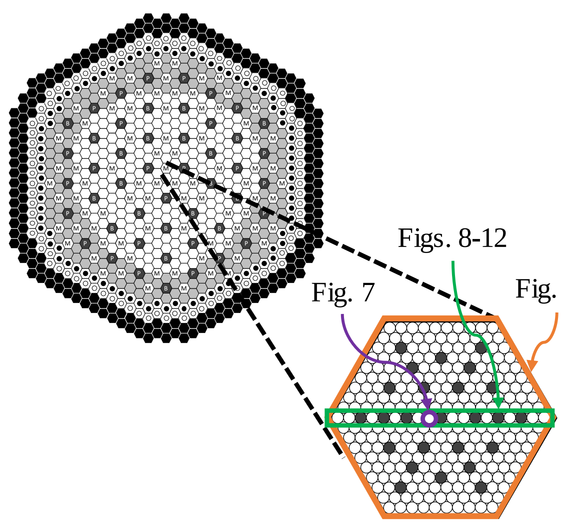


Fig. 6. Location of MA target assembly and pin

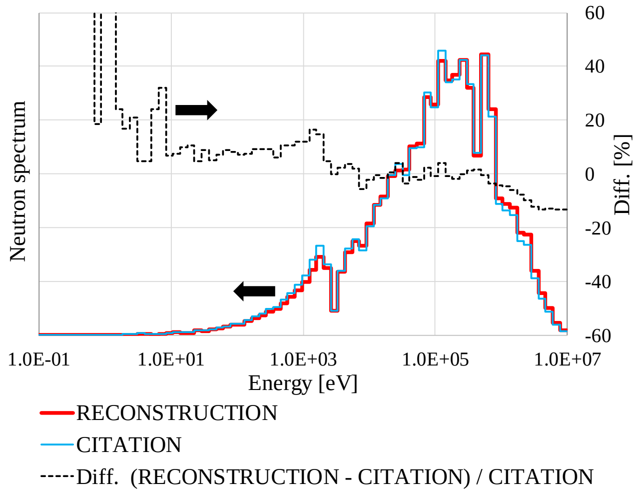


Fig. 7. Neutron spectrum in MA target fuel pin

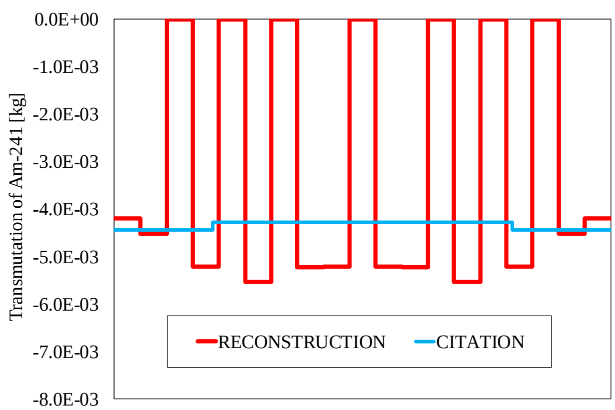


Fig. 8. pin-by-pin transmutation of Am-241

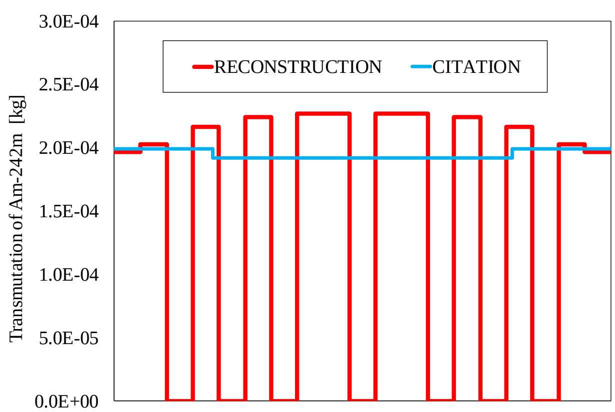


Fig. 9. pin-by-pin transmutation of Am-242m

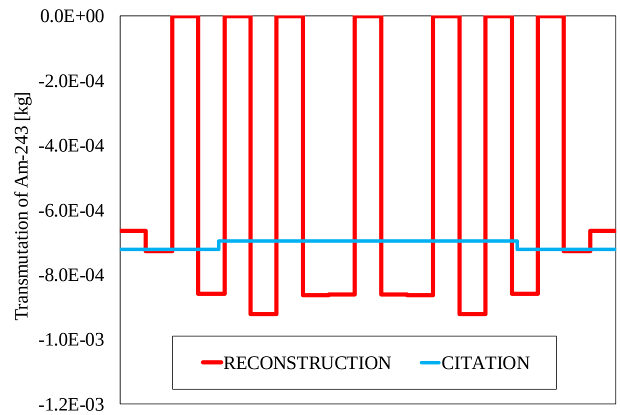


Fig. 10. pin-by-pin transmutation of Am-243

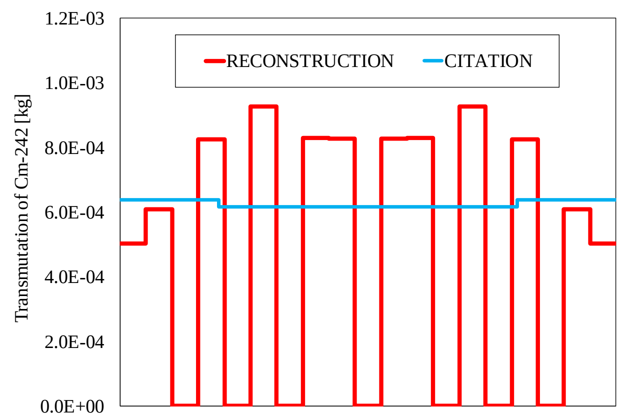


Fig. 11. pin-by-pin transmutation of Cm-242

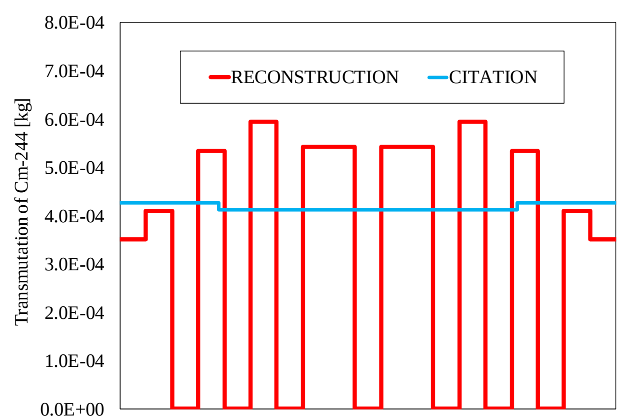


Fig. 12. pin-by-pin transmutation of Cm-244

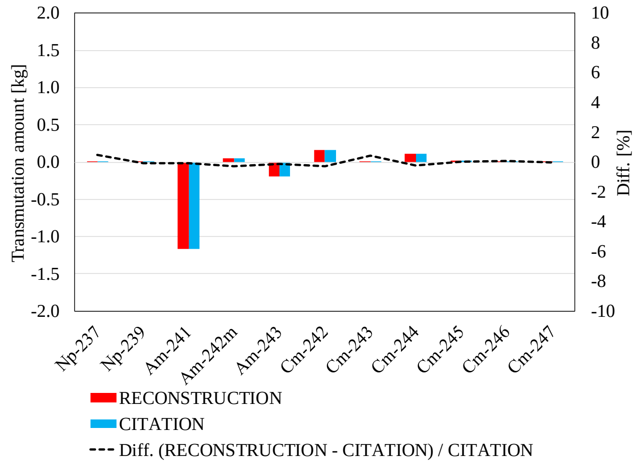


Fig. 13. Comparison of transmutation amount in assembly

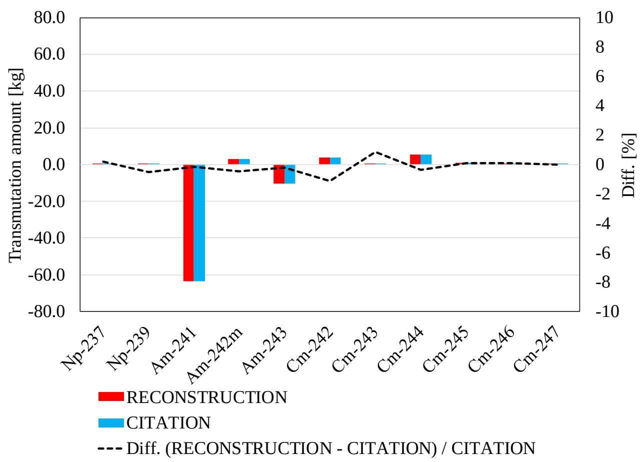


Fig. 14. Comparison of transmutation amount in all MA assembly

V. CONCLUSIONS (HEADING A)

In this paper, the neutron spectrum is evaluated by proposed method which is based on the reconstruction of neutron flux distribution and pin-by-pin MA transmutation is analyzed in heterogeneous MA target loaded core. The results show that the proposed method can evaluate detailed distribution of MA transmutation. At the same time, the difference of total transmutation in an assembly between proposed method and CITATION results is less than about 1%. These results indicate that the impact of reconstruction on total amount of MA transmutation in the core is not remarkable, but the proposed method is efficient for the evaluation of pin-wise MA transmutation.

NOMENCLATURE

$\emptyset$ = neutron flux
V = volume
g = fine energy group
G = collapsed energy group
i = region in assembly

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