

# 論文の内容の要旨

## 論文題目

### Assembly mechanisms of specialized subtypes of the 20S core particle and the lid subcomplex of the proteasome

(プロテアソームの特殊型 20S コア粒子および蓋部の分子集合機構の解明)

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#### [Introduction]

The 26S proteasome catalyzes degradation of ubiquitinated proteins in eukaryotic cells, thus playing a central role in various cellular processes including cell cycle, transcription, signal transduction, immunity, and protein quality control.

The 26S proteasome has a highly complicated structure and is composed of the catalytic 20S core particle (CP) and the 19S regulatory particle (RP), which are assembled from 14 and 19 different subunits, respectively (Figure 1). The standard CP (sCP) consists of 7 different  $\alpha$ -type subunits  $\alpha$ 1-  $\alpha$ 7 and 7 different  $\beta$ -type subunits  $\beta$ 1-  $\beta$ 7, of which  $\beta$ 1,  $\beta$ 2 and  $\beta$ 5 are catalytically active. In vertebrates, two other subtypes of the CP exist. One is the “immunoproteasome (iCP),” in which the catalytic  $\beta$ 1,  $\beta$ 2 and  $\beta$ 5 of the sCP are replaced by another set of catalytic subunits named  $\beta$ 1i,  $\beta$ 2i and  $\beta$ 5i. This iCP efficiently generates antigenic peptides presented on MHC class I molecules. The other is the “thymoproteasome (tCP),” in which  $\beta$ 5i of the iCP is replaced by  $\beta$ 5t, which is exclusively expressed in cortical thymic epithelial cells. This tCP plays a pivotal role in positive selection of CD8<sup>+</sup> T cells. The RP can be divided into a base and a lid subcomplex. The base, which is required for recruiting ubiquitinated proteins and unfolding them, comprises 6 ATPase subunit Rpt1-Rpt6 and four non-ATPase subunit Rpn1, 2, 10 and 13, whereas the lid, which is essential for removing ubiquitin chains from the substrates, comprises 9 non-ATPase subunits Rpn3, 5-9, 11, 12, and 15.

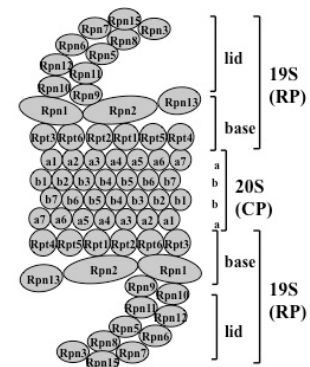


Figure 1. Structure of 26S proteasome

Accurate assembly of the proteasome from the 33 different subunits is a prerequisite for degradation of ubiquitinated proteins. Recent studies have revealed that biogenesis of the sCP and the base subcomplex were assisted by multiple dedicated chaperones. However, little is known about the assembly pathway of the iCP, tCP, and the lid subcomplex. In this study, we investigated the biogenesis of the two specialized types of CPs and the lid subcomplex using combination of RNA interference (RNAi) and mass spectrometry in mammalian cells.

## [Results]

### 1. Dissecting assembly pathways of the 20S immunoproteasome (iCP) and the 20S thymoproteasome (tCP)

1-1. Earlier incorporation of the specialized  $\beta$ -subunits than the standard  $\beta$ -subunits  
 Making use of HeLa cells treated with IFN- $\gamma$  and the stable expression of  $\beta$ 5t in HEK293T cells, we described a series of biochemical experiments employing RNAi of each  $\beta$  subunit, which resulted in accumulation of distinct intermediates. By characterizing these intermediates, we clarified the order of  $\beta$  subunit incorporation in the iCP and tCP. As we showed previously,  $\beta$  subunits were incorporated strictly and sequentially in the order  $\beta$ 2,  $\beta$ 3,  $\beta$ 4,  $\beta$ 5,  $\beta$ 6,  $\beta$ 1, and  $\beta$ 7 in the sCP. However,  $\beta$ 5i and  $\beta$ 5t could be incorporated immediately after the assembly of  $\beta$ 3 even without  $\beta$ 4 in the iCP and tCP, respectively. Furthermore,  $\beta$ 1i and  $\beta$ 2i were incorporated ahead of all the other  $\beta$  subunits (Figure 2).

To elucidate the mechanism of earlier incorporation of  $\beta$ 5i and  $\beta$ 5t compared to  $\beta$ 5, we focused on their propeptides. Two chimeric  $\beta$ 5 subunits were constructed by fusing the propeptide of  $\beta$ 5i or  $\beta$ 5t to the mature form of  $\beta$ 5. Here we refer to these chimeric subunits as  $\beta$ 5i(p)+ $\beta$ 5(m) and  $\beta$ 5t(p)+ $\beta$ 5(m). We expressed these subunits into cells depleted of endogenous  $\beta$ 4 and  $\beta$ 5 and observed whether the chimeric  $\beta$ 5 subunits were incorporated without  $\beta$ 4.  $\beta$ 5i(p)+ $\beta$ 5(m) was not incorporated in the absence of  $\beta$ 4, suggesting that the mature body of  $\beta$ 5i, but not the propeptide of  $\beta$ 5i, was prerequisite for  $\beta$ 5i incorporation (Figure 3). In contrast,  $\beta$ 5t(p)+ $\beta$ 5(m) was readily incorporated without  $\beta$ 4, indicating that the propeptide of  $\beta$ 5t enabled earlier incorporation of  $\beta$ 5 to the premature proteasome (Figure 3).

To sum up, the assembly of the iCP and tCP began with the incorporation of  $\beta$ 1i and  $\beta$ 2i, followed by incorporation of  $\beta$ 3, then  $\beta$ 4 or  $\beta$ 5i/ $\beta$ 5t, and  $\beta$ 6 and  $\beta$ 7 were the last two to be incorporated. In the assembly pathways, the propeptide of  $\beta$ 5t is a key factor for its earlier incorporation than  $\beta$ 4, while the mature form of  $\beta$ 5i is thought to be more crucial to its earlier incorporation. These unique features of  $\beta$ 5t and  $\beta$ 5i may account for preferential assembly of the iCP and tCP over sCP even when standard and specialized subunits are co-expressed.

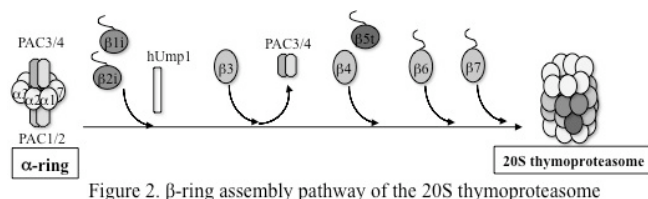


Figure 2.  $\beta$ -ring assembly pathway of the 20S thymoproteasome

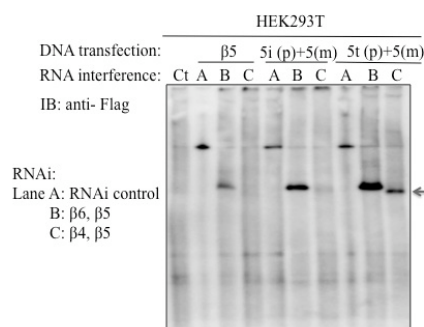


Figure 3. Propeptide of  $\beta$ 5t could assist earlier incorporation of  $\beta$ 5.

## 1-2. Incorporation of $\beta 5t$ is largely dependent on $\beta 1i$ and $\beta 2i$

Since  $\beta 1i$  and  $\beta 2i$  are the common catalytic subunits of iCP and tCP, we examined whether there was any difference in the dependence of  $\beta 5i$  and  $\beta 5t$  incorporation on the presence of  $\beta 1i$  and  $\beta 2i$ .  $\beta 5i$  and  $\beta 5t$  were synthesized with N-terminal propeptides as premature forms. Those propeptides are cleaved upon completion of the CP assembly to expose the catalytic threonine residues, and therefore, processing of the propeptides indicates efficiency of the CP assembly. We expressed  $\beta 5t$  or  $\beta 5i$  in  $\beta 5i$  (-/-) MEF cells. These cells express  $\beta 1i$  and  $\beta 2i$  only when treated with IFN- $\gamma$ . Nearly half of the expressed  $\beta 5t$  were in premature forms without IFN- $\gamma$ , but the mature  $\beta 5t$  was remarkably increased upon IFN- $\gamma$  treatment. In contrast, the majority of  $\beta 5i$  were already matured in the absence of IFN- $\gamma$ , and the induction of  $\beta 5i$  maturation by IFN- $\gamma$  was modest (Figure 4). These results indicated that presence of  $\beta 1i$  and  $\beta 2i$  facilitated incorporation of  $\beta 5t$ , whereas  $\beta 5i$  could be incorporated efficiently in combination with the standard subunits  $\beta 1$  and  $\beta 2$ . This may account for generation of altered TCR repertoire of CD8<sup>+</sup> T cells in  $\beta 1i$ - and  $\beta 2i$ -deficient mice, as reported previously.

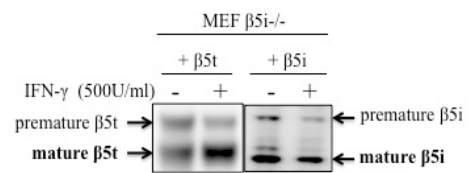


Figure 4. Maturation of  $\beta 5t$  was facilitated by  $\beta 1i$  and  $\beta 2i$ .

## 2. Dissecting assembly pathway of the lid subcomplex

In order to dissect the assembly pathway of the lid subcomplex, we analyzed specific intermediates observed during knockdown of each lid subunit in HEK293T cells by immunoblot and mass spectrometry analysis. When treated with siRNA targeting Rpn12, a complex comprising all the lid subunits except Rpn12 was detected, indicating that Rpn12 was the last subunit incorporated during the lid formation (Figure 5C). When we knocked down Rpn6, two intermediate complexes Rpn3-7 and Rpn5-8-9-11 were observed, suggesting that these two intermediates were formed independently and bound to each other via Rpn6 (Figure 5D). While the association between Rpn3 and Rpn7 was not essential for the stability of either subunit, Rpn5, Rpn8 and Rpn9 were not able to form an intermediate complex without any one of the other subunits, indicating that these three subunits assembled as a set. Additionally, Rpn11 was markedly decreased by knockdown of Rpn5 and Rpn8, indicating that stability of Rpn11 was dependent on the Rpn5-8-9 complex.

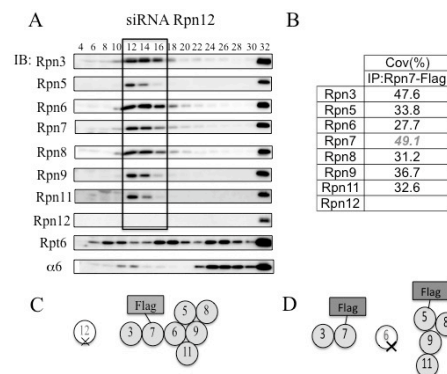


Figure 5. Two intermediates was formed during the assembly, and Rpn12 was incorporated at the final step of the lid formation.

Since no effective antibody against human Rpn15 was available and it was impossible to detect fragmented peptides derived from Rpn15 by our MS analysis due to the detection limit after trypsin digestion, we constructed HEK293T cells stably expressing Rpn15-Venus. An intermediate comprising the lid subunits except Rpn3 and Rpn12 was identified in Rpn15-knockdown cells, and no subunit was co-immunoprecipitated with Rpn15 when we knocked down Rpn3, suggesting that Rpn3 and Rpn15 were assembled into the lid in an interdependent manner.

In brief, an intermediate comprising Rpn5-6-8-9 served as a core module that was prerequisite for assembly of the essential deubiquitinase Rpn11, which then associated with Rpn15-3-7 complex. Rpn12 was the last subunit to be incorporated (Figure 6). The lid formation did not seem to be assisted by any specific chaperones, like CP and the base assembly, because we did not detect molecules other than the lid subunits in the intermediates of lid subcomplex by MS analysis.

### [Discussion]

1. It has been known that pre-CPs containing  $\beta 1i$  and  $\beta 2i$  favored the incorporation of  $\beta 5i$  because  $\beta 5i$  mediated efficient processing of  $\beta 1i$  and enhanced the effectiveness of CP assembly. We showed that incorporation of  $\beta 5t$  was dependent on  $\beta 1i$  and  $\beta 2i$  more than that of  $\beta 5i$  (Result 1-2), and the propeptide of  $\beta 5t$  played an essential role in its incorporation. This feature of  $\beta 5t$  might explain the fact that more than 90% of the CPs is the tCP in cTECs while  $\beta 5t$  and  $\beta 5i$  are transcriptionally co-expressed.
2. Recent research has discovered that overexpression of Rpn6 subunit in *C. elegans* and Rpn11 in fruit fly prolongs the lifespan. It is also shown that FOXO4-mediated upregulation of Rpn6 is a prerequisite for maintaining pluripotency in embryonic stem cells. Overexpression of Rpn11 or Rpn7 is also known to be involved in DNA damage response. However, the mechanisms are still unidentified. Elucidating the assembly pathway of the lid subcomplex should be of help to understand the mechanism in which high expression of a single lid subunit plays such significant roles.

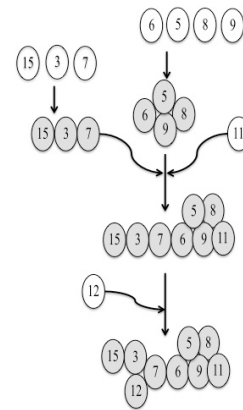


Figure 6. Assembly pathway of the lid subcomplex