speeds up to 5Hz, all subjects perceived color when the rotation speed was greater than or equal to 3 Hz with enhanced effective connectivity between V4 and V1. These results indicate that backward modulation from V4 to V1 plays a significant role to generate subjective color perception during Benham's top illusion.

1P-213 神経回路網における自律活動調整の分子機構

The molecular mechanism of the modulation of the spontaneous activity in a neuronal network

Ai Kiyohara (1), Takahisa Taguchi (2), Suguru Kudoh (3) ((1) School of Science, Osaka University; (2) National Institute of Advanced Industrial Science and Technology (AIST); (3) Division of Human System Interaction, School of Science)

We cultured rat hippocampal neurons on the dish with multi-electrode array and analyzed stage-specific changes of spatio-temporal patterns of network activity. The spatial pattern of spontaneous action potential was analyzed and we found the particular period with transient high frequency bursting (HFB) activity. After termination of HFB, the spatial distribution of the frequency of the action potential became to be widely varied. It was suggested that the neuronal network automatically generated such HFB activity and construct a heterogeneous network, which is appropriate for the information processing.

Various functional molecules are related to synaptic transmission and mechanism of action potential generation, it is likely that the expression of patterns of these molecules influence dynamics of neuronal network. So, the effect of the inhibition of NMDARs was different before and after HFB, suggesting NMDARs were critical for the moderation of the activity pattern. The spatio-temporal pattern of the evoked action potential in the whole neuronal network also greatly depended on the network dynamics expressed in the spatio-temporal pattern of spontaneous activity. We also elucidated the relationship between the spontaneous activity pattern and the pattern of evoked action potential. In the autonomously reconstructed neuronal network, spontaneous activity and evoked activity constituted each state and the spontaneous activity was not the only random background noise.

1P-214 培養神経回路網の長期間発達過程における免疫蛍光染色像と電気活動

Immunofluorescence imaging and electrical activity during long term development of cultured neuronal networks

Takumi Komatsu (1), Daisuke Ito (1), Naohiro Yamada (1), Hiroki Tamate (1), Kazutoshi Gohara (1) ((1) Division of Applied Physics, Graduate School of Engineering, Hokkaido University)

see 1TA3-04

1P-215 固体 NMR によるバクテリオロドプシンの圧力によって誘起されるレチナール異性化機構の解析

Pressure induced retinal isomerization in bacteriorhodopsin as studied by solid-state NMR

Hirohide Nishikawa (1), Kana Tajima (1), Izuru Kawamura (1), Akimori Wada (2), Satoru Tuzi (3), Akira Naito (1) ((1) Graduate School of Engineering, Yokohama National University; (2) Kobe Pharmaceutical University; (3) Department of Life Science, University of Hyogo)

Bacteriorhodopsin (bR) in purple membrane from *H. salinarum* shows a light-driven proton pump activity by photoisomerization of retinal. The retinal configuration in the dark-adapted bR coexists all-*trans* and 13-*cis*, 15-*syn* retinal states with the isomeric ratio close to 1. The population of 13-*cis*, 15-*syn* state can be increased under pressurized condition. In this study, we investigated dynamics of two different retinal configurations in view of ^{13}C chemical shifts, NMR signal intensities and various spin relaxation parameters of ^{13}C retinal in bR by solid state NMR. The 20-C methyl carbon signal intensity of 13-*cis*, 15-*syn* retinal at 22.0 ppm was increased under the fast MAS condition. It is, therefore, indicated that the isomerization from all-*trans* to 13-*cis*, 15-*syn* state was caused by pressure. In addition, the value of ^{13}C spin-lattice relaxation time (T_1) of 13-*cis*, 15-*syn* state is lower than that of all-*trans* state. It is noticed that dynamics of 13-*cis*, 15-*syn* state is more flexible than that of all-*trans* state. These results suggested that a molar volume change of protein with retinal isomerization was caused by pressure. We will discuss about the change of retinal-protein interaction and protein structure caused by pressure.

1P-216 ^{13}C 固体 NMR によるバクテリオロドプシンの Tyr コンフォメーション変化の解析

Conformational changes at Tyr residues in Bacteriorhodopsin as studied by high-resolution ^{13}C solid state NMR

Izuru Kawamura (1), Miyako Horigome (1), Junko Tanabe (1), Masato Omine (1), Satoru Tuzi (2), Akira Naito (1) ((1) Yokohama National University; (2) University of Hyogo)

Bacteriorhodopsin (BR) is a membrane protein containing retinal which shows functions as a light-driven proton pump. It is important to understand how retinal configurations activate protein through retinal-protein interactions. We investigated dynamic structure of BR corresponding to each of the retinal configurations by solid-state NMR spectroscopy. Backbone carbonyl carbon signals of Tyr26, 57, 64, 79, 131, 133, 147, 150 and 185 in BR were uniquely observed and assigned to each Tyr residues by REDOR technique at 293K. In particular, two ^{13}C NMR peaks were observed for Tyr57, 79, 133 and 185, respectively in REDOR-filtered spectra. It is, therefore, revealed that these two peaks of Tyr57, 79, 133, 185 were attributed to the BR with all-*trans* and 13-*cis*, 15-*syn* retinal configurations in the dark [1]. Consequently, the two major peaks at 176.0 and 174.0 ppm in ^{13}C CP-MAS NMR spectrum of [^{13}C]Tyr BR were assigned to all-*trans* and 13-*cis*, 15-*syn* state respectively. The two peaks were also altered to exhibit a broad singlet pattern after retinal was removed [2]. Therefore, our results indicate that protein conformations of retinal binding site are different from extracellular surface corresponding to two retinal configurations in the dark. We will discuss the temperature variation of protein conformational change.

[1] I. Kawamura et al. (2007) *J. Am. Chem. Soc.* 129 1016-1017.

[2] I. Kawamura et al. (2007) *Biochim. Biophys. Acta* 1768 3090-3097.

1P-217 固体 NMR による光受容タンパク質 ppR とその変異体 T204A の局所構造変化の解析

Analysis of local protein conformations in photoreceptor ppR and its mutant T204A by solid-state NMR

Tetsuro Hidaka (1), Izuru Kawamura (1), Takudo Nishio (1), Kazuhiro Osawa (1), Naoki Kamo (2), Akira Naito (1) ((1) Graduate School of Engineering, Yokohama National University; (2) College of Pharmaceutical Sciences, Matsuyama University)

see 1TP2-01

1P-218 固体 ^{13}C NMR による ppR の細胞質表面部位の相互作用変化の観測

Change of interaction in cytoplasmic surface region of ppR with pHtrII in the complex formation as studied by solid-state NMR

Takahiro Kondo (1), Izuru Kawamura (1), Takudo Nishio (1), Naoki Kamo (2), Akira Naito (1) ((1) Graduate School of Engineering, Yokohama National University; (2) Graduate School of Pharmaceutical Sciences, Hokkaido University; College of Pharmaceutical Sciences, Matsuyama University)

Pharaonis phoborhodopsin (ppR) is a negative phototaxis receptor from *Natronomonas pharaonis* and forms a complex with its cognate transducer pHtrII. To understand molecular mechanism of negative phototaxis, it is important to observe the interactional changes of ppR with pHtrII during complex formation and photo activation processes. In this study, interaction of ppR with pHtrII in the cytoplasmic side was examined using solid-state NMR. [^{13}C] Ser and [^{13}C] Ala-labeled ppR and its complex with pHtrII(1-159) were prepared to investigate the interaction because Ser are mainly locate in the cytoplasmic surface region and Ala are located in the wide region of ppR. In the ^{13}C DD-MAS NMR spectra of [^{13}C] Ala-labeled ppR and ppR-pHtrII complex, ^{13}C NMR signal intensity of the C-terminal region of ppR decreased in comparison to that of ppR alone [1]. Similarly ^{13}C NMR signal at 171.8ppm of [^{13}C] Ser-labeled ppR complexed with pHtrII also decreased. The signal at 171.8ppm can be assigned to Ser226 in the C-terminal tip. Therefore it turned out that the C-terminal region in ppR participate in complex formation with pHtrII. The change of these signals on photo-activated ppR will be discussed in process of the interaction switch of ppR with pHtrII as compared with D75N-pHtrII complex [1].

[1] I. Kawamura et al. Photochem. Photobiol. (2008) 84,921-930.

1P-219 HAMP ドメインの分子動力学解析：電子スピン常磁性共鳴のデータを満足する 4-helix bundle 構造

Molecular dynamical analysis of a HAMP domain: A four-helix bundle structure satisfies the data of electron paramagnetic resonance

Koro Nishikata (1), Sotaro Fuchigami (2), Mitsunori Ikeguchi (2), Akinori Kidera (3) ((1) Supramolecular Biology, International Graduate School of Arts and Sciences, Yokohama City University; (2) Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University; (3) Department of Supramolecular Biology, Graduate School of Nanobioscience, Yokohama City University; Research Program for Computational Science, RIKEN)

see 1TP2-02