Mechanism of Optical Rotation of Amino Acids Using Electronic State Calculation

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Abstract. Because of the chiral nature of the building blocks of living matter, an optical phenomena associated with the chirality constitute an important topic in physical chemistry. The specific optical rotation, which is a parameter for the characterization of the natural optical activity, depends strongly on the conformation of the molecule. In this study, we investigated the dependence of the optical rotation on a molecular conformation in the gas phase by calculating the electronic states of seven kind of chiral amino acids using the DV-Xα method. As a result, we can confirm the existence of an antibonding orbital on the side chain and the optical rotations are strongly related.

1. Introduction
Optical rotation is a physical property that causes linearly polarized light to rotate left or right when it passes through a substance, and many biological substances such as proteins and sugars exhibit the optical rotation. Furthermore, enantiomers such as L-alanine and D-alanine have the property that most of the physical and chemical properties are the same, except for the sign of the optical rotation.
On the other hand, with regard to biological properties, one enantiomer may be a drug and the other a poison such as thalidomide. Therefore, identification of the enantiomers is an important factor, and optical rotation is a key to determine the conformation of a chiral molecule. However, there are few theoretical studies of the optical rotation mechanism, and it is hard to say that everything is clear.

Therefore, in this study, it is assumed optical rotation is caused by spirality of charge density located on asymmetric carbon, and electronic state calculation was performed on amino acids that show optical rotation while having a simple molecular structure. After that, comparison with experimental values was performed.

2. Method

In this study, a software “Chem3D” was used to create a computational model of 15 kinds of amino acids with only one asymmetric carbon. Based on the calculation model, we used the DV-\(\alpha\) molecular orbital method to calculate the BOP of the bond to the asymmetric carbon and the overlap of the bonding orbitals and the antibonding orbitals. Here, since the spin direction is reversed due to the presence of the antibonding orbital, the spirality of the space charge density is considered to be reversed, and this is used as an index of optical rotation. From the calculation results obtained, the areas of overlap of all antibonding orbitals around HOMO, LUMO, and less than HOMO were plotted and compared in order of experimental optical rotation.

3. Results and Discussion

Table 1 shows the experimental values of the optical rotation (\([\alpha]_D\)) of amino acids calculated in this work and the calculated BOP values. Next, from the results obtained from the overlap population diagram, the area of the antibonding orbital around the HOMO is extracted and shown in Figure 1. Similarly, Figure 2 shows the results at around LUMO, and Figure 3 shows all overlaps results below HOMO. The horizontal axis of each graph plots the experimental value of an optical rotation, and the vertical axis plots the area of each corresponding antibonding orbital.

According to the result in Table 1, it can be seen the values of BOP at the asymmetric carbon of each amino acid take similar values. From this, it seems difficult to explain the factor of different optical rotation by the value of BOP.

Next, according to the result in Figure 1, around LUMO, antibonding orbitals exist for hydrogen and carboxyl groups, but there is almost no antibonding orbital for side chains and amino groups. It can be seen the contribution to the side chain of the antibonding orbital due to the change in the side chain of the amino acid is small, affecting others.

In Figure 2, the antibonding orbital of the amino group which didn't influence in Figure 1 is largely shown around LUMO. As a result of component analysis, it is found that the antibonding orbital appears around the HOMO of the amino group due to the 2s orbital of the amino group and the 2p
orbital of the asymmetric carbon. There is no side chain effect on this, and it is thought an antibonding orbital always exists between the amino group and the asymmetric carbon around the HOMO of the amino acid.

Finally, as shown in Figure 3, it is found the overlap of antibonding orbitals is divided into four regions shown by the highlighted ellipsoid, in the order of hydrogen, side chain, carboxyl group and amino group. Furthermore, as the dextrorotatory property increases, the overlap of the antibonding orbitals between the carboxyl group and the side chain increases. This is considered to be due to the fact the spirality of the charge in the right rotation is increased by the antibonding orbital. However, in this study, it couldn't confirm the switch of levorotatory to dextrorotatory or dextrorotatory to levorotatory from the change in the antibonding orbital.

**Table 1.** Experimental optical rotation values and BOP values of amino acids.

| substance       | $-\text{R}$ | [$\alpha_\text{D}$ in H$_2$O] | N(-NH$_3$) | C(-COOH) | C(-R) |
|-----------------|--------------|-------------------------------|-----------|----------|-------|
| L-cysteine      | CH$_2$SH     | -16.5                         | 0.693     | 0.759    | 0.733 |
| L-leucine       | CH$_3$CH(CH$_3$)$_2$ | -11                      | 0.686     | 0.748    | 0.744 |
| L-methionine    | CH$_3$CH$_2$SCH$_3$ | -10                      | 0.690     | 0.758    | 0.738 |
| L-serine        | CH$_3$OH     | -7.5                         | 0.701     | 0.756    | 0.743 |
| L-asparagine    | CH$_3$CONH$_2$ | -5.6                       | 0.700     | 0.759    | 0.741 |
| L-alanine       | CH$_3$       | +1.8                         | 0.676     | 0.754    | 0.753 |
| L-norleucine    | CH$_3$CH$_2$CH$_2$CH$_3$ | +4.7                      | 0.689     | 0.751    | 0.736 |
| L-aspartic acid | CH$_2$COOH   | +5.05                        | 0.689     | 0.760    | 0.735 |
| L-valine        | CH(CH$_3$)$_2$ | +5.6                       | 0.692     | 0.758    | 0.738 |
| L-glutamine     | CH$_2$CH$_2$CONH$_2$ | +6.3                      | 0.684     | 0.763    | 0.733 |
| L-norvaline     | CH$_2$CH$_2$CH$_3$ | +7.0                       | 0.698     | 0.765    | 0.740 |
| L-amino butyric acid | CH$_3$CH$_2$ | +9.3                         | 0.700     | 0.765    | 0.735 |
| L-glutamic acid | CH$_3$CH$_2$COOH | 12                       | 0.698     | 0.750    | 0.735 |
| L-ornithine     | CH$_3$CH$_2$CH$_2$NH$_2$ | 12.1                      | 0.698     | 0.750    | 0.739 |
| L-arginine      | CH$_3$CH$_2$CH$_2$NH(CNH)NH$_2$ | 12.5                      | 0.679     | 0.751    | 0.735 |
Figure 1. Relationship between the optical rotation value and the antibonding orbital around the HOMO.

Figure 2. Relationship between the optical rotation value and the antibonding orbital around the LUMO.
Figure 3. Relationship between the optical rotation value and the antibonding orbital below HOMO.

4. Conclusion
In this study, in order to clarify the mechanism of optical rotation, we calculated the electronic states of amino acids having only one asymmetric carbon, confirmed the BOP and each overlap population diagrams, and confirmed their relationship with optical rotation. From the calculation results, it was possible to confirm the regular change in the antibonding orbital by the change in the side chain of amino acids. In the future, we will consider the influence of the size of the bonding orbital, and calculate the case where the amino acid is zwitterion. Moreover, we'll examine whether the effect on physical properties can predict according to the calculation by collecting data.

References
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